## **SEARCH REQUEST FORM**

Requestor's Name:		Serial Number:	
Date:	Phone:	Art Unit	:
Search Topic: Please write a detailed statement of sear that may have a special meaning. Give a copy of the sequence. You may incl	examples or relevant citations, a	uthors keywords, etc., if known.	
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	STAFF USE (	ONLY	
Date completed: 05-13-0  Searcher: Belleving 6  Terminal time: 20  Elapsed time: 23  Number of Searches: Number of Databases: 1	Search  2499 4  Type 0	Site         V           STIC	endors  IG Suite  STN  Dialog  APS  Geninfo  SDC  DARC/Questel  Other

PTO-1590 (9-90)

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Database
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Gapop 10.0 , Gapext 0.5
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ABB05253
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AAY71083
AAM79380
AAM78396
ABP41342
AAB93319
AAE01176
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1422.450 Million cell updates/sec
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Mouse B-aggressin Human protein SEG Human protein SEG Human protein ant Human protein sec Human gene 13 enc
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Human transcript
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AAY71082
ID AAY7
XX
AC AAY7
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DT 29-A
XX
DE Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human B-aggressive lymphoma (BAL) protein
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Arabidopsis thalia		21	151	3.2	144
breast canc		22	907	ω ω	145
Human tankyrase2 e		22	1099		46.5
Staphylococcus aur		22	716		148
Human AFP protein		22	125		148
Human colon cancer		22	173	ω	151
		22	1166	ω •	.54.5
		22	487	ω.	156
Human TETRA polype		22	220	ω	156
Human cancer assoc		21	378	ω	157
Drosophila tankyra		22	1181	ω	.57.5
Drosophila melanog		22	1181	ω	57.5
Amino acid sequenc		22	373	ω	159
Human histone fusi		20	373	ω	159
Human protein sequ		22	372	ω	61.5
Human polypeptide		22	542	4.	177
Human bone marrow		22	188	4.	187
	PAE01226 -	22	200		187.5
protein s		22	386	4.	189
Human secreted pro		22	386	4	189
Human protein SEQ		22	357	4.	189
Protein regulating		21	226	4	189
Arabidopsis thalia		21	239	4.	96.5
		21	200	4	96.5
ORFX		21	368	4	197
ORFX		21	187	4	201
prot		22	363	4.	203
y injury ass		20	168	4.	04.5
poly(ADP-		23	1025		211.5
Human protein sequ		22	1025	4.8	11.
ium		22	246		219 -
ria monocyto	ABB4935	23	176		235
ein se	AAB9405	22	419		256
otoga mariti	ABB84807	23	599	6.6	291.5
	ABG6406	23	4		363

## ALIGNMENTS

sequ FT eucaryotes"	i FT	FT	FT	sive FT /note= "contains a duplicated domain c	otio FT Region . 335447	on-i FT eucaryotes"	on in a family of related proteins fro	sive . FT macro H2A, non-structural polyproteins	which is found in the non-histone regi	FT /note= "contains a duplicated domain o	FT Region 136256	FT /note= "Alternatively spliced sequence"	FT Region 1751	FH Key Location/Qualifiers	××	OS Homo sapiens.	XX	KW cellular adhesion; sarcoma; carcinoma; myeloma.	KW cytostatic; vaccine; treatment; diagnosis; non-Hodgkin's lymphoma;	KW differential expression; DLB-CL; Diffuse large B-cell lymphoma;	KW Human; B-aggressive lymphoma; BAL; chromosome 3q21; tumour; malignancy;	
	or in a family of related proteins from bacteria to	macro H2A, non-structural polyproteins of ssRNA viruses	which is found in the non-histone region of histone	/note= "contains a duplicated domain of unknown function			or in a family of related proteins from bacteria to	non-structural polyproteins of ssRNA viruses	which is found in the non-histone region of histone	/note= "contains a duplicated domain of unknown function		ernatively spliced sequence" ·		llifiers			-	carcinoma; myeloma.	ent; diagnosis; non-Hodgkin's lymphoma;	3-CL; Diffuse large B-cell lymphoma;	<ol> <li>BAL; chromosome 3q21; tumour; malignancy;</li> </ol>	

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Best Local Similarity
                                                                                                                          Matches
                                                                                                                                                                                                                                large B-cell lymphoma), the most common non-Hodgkin's lymphoma, by differential display technique. It was found to be more abundant in tumours from patients with high risk fatal DLB-CL disease than low risk cured disease. BAL transcripts are most abundant in lymphoid organs e.g. spleen, foetal liver and peripheral blood, and several non-haematopoieti organs e.g. heart and skeletal muscle. BAL is involved in modulation of cellular adhesion and aggressiveness/severity of malignancy such as DLB-CL. BAL nucleic acid and protein are useful for identifying cells exhibiting or predisposed to malignancies such as lymphoma, sarcoma, carcinoma and myeloma. BAL proteins are useful as immunogens to raise anti-BAL antibodies. BAL modulators or BAL molecules can be used for
                                                                                                                                                                                               prophylactic and therapeutic treatment of a subject susceptible to or having a disorder associated with aberrant BAL expression or activity such as non-Hodgkin's lymphoma. It is also useful in vaccine preparati
                                                                                                                                                                                                                                                                                                                                                                    protein obtained by screening two human cDNA libraries derived from anti-immunoglobulin activated splenocytes and the Raji Burkitts lymphoma cell line cloned into pCDM8. The BAL locus is mapped to chromosome 3q21. BAL was identified to be differentially expressed in DLB-CL (Diffuse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New B-aggressive lymphoma nucleic acid for identifying cells exhibiting or predisposed to malignancies such as lymphoma, saccoma, carcinoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAD00629
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30-OCT-1998;
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121 SVWKDDLTTHAVDAVVNAANEDLLHGGGLALALVKAGGFEIQEESKQFVARYGKVSAGEI
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                                                                                     MDFSMVAGAAAYNEKSGRITSLSLLFQKVFAQIFPQWRKGNTEECLPYKCSETGÅLGENY
                                    SWQIPINHNDFKILKNNERQLCEVLQNKFGCISTLVSPVQEGNSKSLQVFRKMLTPRIEL
                        SWQIPINHNDFKILKNNERQLCEVLQNKFGCISTLVSPVQEGNSKSLQVFRKMLTPRIEL
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781.786
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Human interferon-induced tetraspan (IIT) protein
                                           Modified-site
                                                                                                                                                                          immunosuppressive; antiinflammatory gene therapy; autoimmune disease;
inflammatory_disease; cardiovascular disease; metabolic disease;
                                                                                                                                                                                                                        Human; interferon-induced tetraspan; IIT; cytostatic; anti-HIV;
                                                                                                                                                                                                                                                                                                                    10-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                          ABB05392 standard; Protein; 819
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                                                                                                                                                        growth
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                                                                                                                                                        inhibition;
Location/Qualifiers 24..26 /note- "Asn is N-gly 69..71
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                    "Asn is N-glycosylated"
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Best Loc
Matches
                                                                                                                                         The present sequence represents a human interferon-induced tetraspan (III) protein (I). (I) has cytostatic, anti-IIV, immunosuppressive and antiinflammatory activities. The polynucleotide (II) encoding (I) can be used in gene therapy. (I) and (II) can be used for treating or preventing a pathology associated with (I) in a subject, preferably human, or for the manufacture of a medicament for treating a syndrome associated with a human disease selected from a pathology associated with (I). (I) and (II) can be used for treating autoimmune diseases, inflammatory diseases, cardiovascular diseases, metabolic diseases, and for inhibiting cancer growth and metastasis. (I) or (II) can be used as diagnostic and/or prognostic markers, in gene therapy, as research tools, and for tissue regeneration in vitro and in vivo.
                                                                                                                                                                                                                                                                                         Novel isolated interferon-induced tetraspan polypeptide, useful treating autoimmune, inflammatory, cardiovascular and metabolic diseases, and for inhibiting cancer growth and metastasis -
                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                               (CURA-)
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DB; ABA93022.
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RESULT 3
ABB05391
                   immunosuppressive; antiinflammatory gene therapy; autoimmune disinflammatory disease; cardiovascular disease; metabolic disease; cancer growth inhibition; metastasis.
                                                                                                              Human interferon-induced tetraspan (IIT) protein #1.
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Homo sapiens
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Location/Qualifiers 417..419

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"encoded by ACATTT"

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Best Loc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated interferon-induced tetraspan polypeptide, useful treating autoimmune, inflammatory, cardiovascular and metabolic diseases, and for inhibiting cancer growth and metastasks -
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NITSISFPALGTGNMEIKKETAAEILFDEVLTF-AKDHVKHQLTVKFVIFPTDLEIYKAF
                                                            KSEFLATKAKQFQRSQLVLVTKGFNLFCKYIYHVLWHSEFPKPQILKHAMKECLEKCIEQ
                                                                                                                                            LGQETTPSENAMVVNNLTLQIVQGHIEWQTADVIVNSVNPHDITVGPVAKSILQQAGVEM
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DB; ABA93022.
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BIOGEN INC.
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The present sequence is the protein sequence for a human transcription factor. The transcription factor and its coding sequence are useful in the diagnosis, treatment and prevention of diseases associated with altered expression of the transcription factor e.g. cell proliferative autoimmune/inflammatory, neurological and developmental disorders. A

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Azimzai Y,
                                                                                                                                                                                                                                                                                                                Human; transcription factor; TRFX; cell proliferative disease; autoimmune disease; inflammation; neurological disease; developmental disorder; cancer; AIDS; infection; cytostatic; a
                                                                          Novel transcription factor polypeptides, used to associated with altered activity and expression of for agents capable of modulating its activity.
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                                                          Claim 1; Pages
                                                                                                                   N-PSDB;
                                                                                                                            WPI; 2001-570896/64
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                                                                                                                                      AAY71083;
               differential
                               Mouse; B-aggressive lymphoma; BAL; tumour;
                                                                 Mouse B-aggressive lymphoma
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                                                                                                                                                                                                                                                                         PETFVIFSGMQAIPQYLWTCTQEYVQSQDYSSGPMRPFAQHPWRGFASGSPVD
                                                                                                                                                                                                                                                                                                                        LKNLAEKAKKISAADKLIYVFEAEVLTGFFCQGHPLNIVPPPLSPGAIDGHDSVVDNVSS
                                                                                                                                                                                                                                                                                                                                                                                          AFQRKKKMMEEKLHRQPVSHRLFQQVPYQFCNVVCRVGFQRMYSTPCDPKYGAGIYFTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLGQWTIQQQKTQDEMKENIIFLKCPVPPTQELLDQKKQFEKCGLQVLKVEKIDNEVLMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAEILFDEVLTFAKDHVKHQLTVKFVIFPTDLEIYKAFSSEMAKRSKMLSLNNYSVPQST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQGHIEWQTADVIVNSVNPHDITVGPVAKSILQQAGVEMKSEFLATKAKQFQRSQLVLVT
                                                                                                                                                                                                                                                     PETFVIFSGMQAIPQYLWTCTQEYVQSQDYSSGPMRPFAQHPWRGFASGSPVD 653
                                                                                                                                                                                                                                                                                                                                                                                                                          AFQRKKKMMEEKLHRQPVSHRLFQQVPYQFCNVVCRVGFQRMYSTPCDPKYGAGIYFTKN 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSQLQKTSSVSITEIISPGRTELEIEGARADLIEVVMNIEDMLCKVQEEMARKKERGLWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specific disorders/diseases are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
               expression; DLB-CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                    Protein;
                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.2%;
treatment; diagnosis;
                                                                                                                                                                    826
                                                               (BAL) protein-short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 3388; DB 22;
Pred. No. 1.2e-278;
D; Mismatches. 1;
                                                                                                                                                                    AA
                 Diffuse
               large B-cell
non-Hodgkin's
                              malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the specification,
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               Lymphoma;
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220 122 160

ILNYVIYKNTHIKTVAIPALSSGIFQFPLNLCTKTIVETIRVSLQGKPMMSNLKEIHLVS EIQEESKRIIANVGKISVGGIAITGAGRIPCHLIIHAVGPRWTVTNSQTAIELLKFAIRN EIQEESKQFVARYGKVSAGEIAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTGKLQRAIVS 219

181

Q Db

62

 ${\tt AGSSSPAQRVFRRTLIPGIELSVWKDDLTRHVVDAVVNAANENLLHGSGLAGSLVKTGGF}$ 

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                                                                                                                                                        Matches. 508;
                                                                                                             Query Match
Best Local
                                                                                                                                                                                             organs e.g. heart and skeletal muscle. BAL is involved in modulation of cellular adhesion and aggressiveness/severity of mallgnancy such as DLB-CL. BAL nucleic acid and protein are useful for identifying cells exhibiting or predisposed to mallgnancies such as lymphoma, sarcoma, carcinoma and myeloma. BAL proteins are useful as immunogens to raise anti-BAL antibodies. BAL modulators or BAL molecules can be used for prophylactic and therapeutic treatment of a subject susceptible to or having a disorder associated with aberrant BAL expression or activity.
                                                                                                                                                                                                                                                                                                              The present sequence is a short form of B-aggressive lymphoma (BAL) protein obtained from mouse (BALb-c) spleen. BAL was identified to be differentially expressed in DLB-CL (Diffuse large B-cell lymphoma), the most common non-Hodgkin's lymphoma, by differential display technique. It was found to be more abundant in tumours from patients with high risk fatal DLB-CL disease than low risk cured disease. BAL transcripts are most abundant in lymphoid organs e.g spleen, foetal liver and peripheral blood, and several non-haematopoiet.
                                                                                                                                                                                  such as non-Hodgkin's lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New B-aggressive lymphoma nucleic ac
or predisposed to malignancies such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
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30-OCT-1998;
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                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myeloma
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                                                        41 NTEECLPYKCSETGALGENYSWQIPINHNDFKIIKNNERQLCEVLQNKFGCISTLVSPVQ
                                         N
EGNSKSLQ-VFRKMLTPRIELSVWKDDLTTHAVDAVVNAANEDLLHGGGLALALVKAGGF
                                         DTWAAAPAERPANNSLEEHYRWQIPIKHNVFEILKSNESQLCEVLQNKFGCISTLSCPTL 61
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                                                                                                               Similarity
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                                                                                                                                                        826
                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            2; 151pp; English
                                                                                                                                                        AA;
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98US-0106448.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   macro-H2A.1 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Proline_rich_domain
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                                                                                                            55.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yakushijin
                                                                                                 96;
                                                                                              Score 2453; DB 21;
Pred. No. 4.5e-199;
6; Mismatches 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INC.
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lymphoma, sarcoma,
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                                                                                                                         Length
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03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
                                                                                       05-FEB-2001;
                                                                                                               09-AUG-2001
                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                 vaccine;
                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                           06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                            AAM79380 standard;
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                                                                                                                                                                                                                                                                                                                                                                                     QAMPLYLWTCTQDRTFSQHPMWSQDYSSGPGMVSSLQSWEWVLNGSSV
                                                                                                                                                                                                                                                                                                                                                                                                    QAIPQYLWTCTQEY-----VQSQDYSSGPMRPFAQHPWRGFASGSPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LWHSEFPKPQILKHAMKECLEKCIEQNITSISFPALGTGNMEIKKETAAEILFDEVLTFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TSSTDKLIYVFEAEVLTGSFCQGNSSNIIPPPLSPGALDVNDSVVDNVSSPETIVVFNGM
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                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                     cytokine; cell proliferation; cell different
e; peptide therapy; stem cell growth factor;
growth factor; immunomodulatory; cancer; let
s system disorder; arthritis; inflammation.
2000US-0496914.
2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0663561.
                                                                                      2001WO-US04098
                                                                                                                                                                                                                                                    SEQ ID
                                                                                                                                                                                                                                                                                                                            Protein;
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                                                                                                                                                                                                                                                    3026.
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                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                         cell differentiation;
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leukaemia;
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                                                                                                                RESULT
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Matches
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Zhao QA,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM8302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammation.
Note: Records for SEQ ID NO 2110 (AAK52581),
(AAM80020) are omitted as the relevant pages
were missing at the time of publication.
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                                    06-NOV-2001
                                                                                     AAM78396 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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30-NOV-2000; 2000US-0728422
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Yang Y, Wejhrman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polynucleotides and polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                        of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, ar metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, related to the control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorges gastrointestinal disorder; urinary system disorder; drug screenif gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotectiantinflammatory; gynaecological; reproductive.
immunodeficiencies, autoimmunė oophoritis, systemic lupus erythema blood-related disorders (e.g., anaemia), cardiovascular disorders respiratory disorders, neurological disorders, gastrointestinal diand urinary system disorders. Ovarian antigen polypeptides and
                                                                                                                                                                                                                       polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., Chlamydla, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ovarian cancer; breast cancer; reproductive sy
infertility; pregnancy disorder; anovulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11;
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DB; ABQ54419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ
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                                                               disorders
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
    Claim
                                                                                                                                                                                                  11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                              29-JUL-1999;
27-AUG-1999;
                           full-length
                                                                                           WPI; 2001-318749/34.
                                                                                                                                                                                       09-JUN-2000;
                                                                                                                                                                                                                                                                     28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                 07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               Human; primer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVNPHDITVGPVAKSILQQAGVEMKSEFLATKAKQFNGPSWYWSQKDL-TXSVNIYTMY
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 8; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                 Isogai T,
                                                                                                                    Sugiyama
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; 2000JP-0183767.
; 2000JP-0241899.
                              CDNAS
  ID 12406;
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                             detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                              99JP-0248036
99JP-0300253
                                                                                                                    Nishikawa T,
T, Wakamatsu
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2537pp +
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Pred. No. 2.8e
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA
                                                                                                                    Hayashi K,
ı A, Nagai K
    ROM;
                                                                                                                      Nagai K,
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2.8e-85;
hes 9;
 English
                                                                                                                                  Saito
                                                                                                                    Otsuki
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                                                                                                                                  Yamamoto J;
                                        detection by the
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH03168 to AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the complementary strand of a polynucleotide which comprises one of the 502 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
520
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                                      615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 TADVIVNSV-NPHDITVGPVAKSILQQAGVEMKSEFLATKAKQFQRSQLVLVTKGFNLFC
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QΕ
                                      ΚE
                                                                               DEKEYQELNELQKKLNINIS--LDHKRPLIKVLGISRDVMQARDEIEAMIKRVR--LAKE
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                                                                                                                   GRKEHDILSQLQKTSSVSITEIISPGRTELEIEGARADLIEVVMNIEDMLCKVQEEMARK
                                                                                                                                                                                                                                                                                                                                                                        KYIYHVLWHSEFPKPQILKHAMKECLEKCIEQNITSISFPALGTGNMEIKKETAAEILFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLSLKSTAFPATGTGNLGFPKNTFAELITSEV-FKFSSKNQLKTLQEVHFLLHPSDHENT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTHIKTVAIPALSSGIFQFPLNLCTKTIVETIRVSLQGKPMMSNLKEIH--LVSNEDPTV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARYGKVSAGEIAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTGKLQRAIVSILN--YVIYK
                                                                                                                                                                                                   PQSTREEKRENGLEAR---SPAINLMGENVEEMYEAHAWIQRILSL-QNHHILENNHILYL
                                                                                                                                                                                                                                             AIEDFVQKGSAQSVKKVKVVIFLPQVLDVFYANMKKREGTQLSSQQSVMSKLASFLGFS-
                                                                                                                                                                                                                                                                                      EVLTFA-KDHVKHQLTVKFVIF-PTDLEIYKA-----FSSEMAKRSKMLSLNNYSV
                                                                                                                                                                                                                                                                                                                               KNIIHVIGGND-----VKSSVSSVLQECEKKNYSSICLPAIGTGNAKQHPDKVAEAIID
                                                                                                                                                                                                                                                                                                                                                                                                                EADVIVNSTSNSFNLKAG-VSKAILECAGQNVERE---CSQQAQQRKNDYIITGGGFLRC
                                                                                                                                                            -KQSPQKKNHLVLEKKTESATFRVCGENVTCVEYAISWLQDLIEKEQCPYTSEDECIKDF
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                                      616
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26.6%;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
L.2e-26;
hes 220;
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RESULT 10 AAE01176

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09-NOV-1999;
07-APR-2000;
27-JUL-2000;
                                                                                          AAD05053-AAD05106 represent cDNAs corresponding to 15 human secre protein genes, and AAE01164-AAE01217 represent the proteins they AAE01218-AAE01226 represent human secreted protein fragments or value secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or therapy. Pathological conditions can be diagnosed by determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; proriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                   proliferative disorders, cancer, tumours abnormalities, haematopoietic disorders,
                                                                                                                                                                                         Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gastrointestinal disorder; pregnancy-related disorder;
endocrine disorder; infection; wound healing; vulnerar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE01176 standard;
                                                                                                                                                                                                                            Isolated nucleic acid
                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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immune system disorder; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUL-2001
                                           ant of the new protein in a sample or by determining the presence of ations in the new genes. Specific uses are described for each of the genes, based on the tissues in which they are most highly expressed, include developing products for the diagnosis or treatment of
                                                                                                                                                                                                             in preventing,
                                                                                                                                                                                                                                                                 2001-308780/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene 13 encoded secreted protein clone HRABS65,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    partner identification.
                                                                                                                                                                                     Page 451-453; 474pp; English
                                                                                                                                                                                                                                                                                         Komatsoulis
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2000US-0195296.
2000US-0221367.
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                                                                                                                                                                                                                                                                                                                                                                                            2000WO-US30039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
97
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98
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95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 444
                                                                                                                                                                                                            id molecule of treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   developmental abnormality; haematopoietic disorder;
der; AIDS; autoimmune disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                       G,
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tumours, Ioecas of the sorders, diseases of the channatoid arthritis),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGG"
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                                                                                                                                                                                                                                                                                         Ebner
                                                                                                                                                                                                                         Ф
                                                                                                                                                                                                             human secreted protein 
ing a medical condition
                               foetal and developmental
                                                                                                                                                                                                                                                                                       ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vulnerary; gene therapy;
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                                                                                                                                   proteins they encode. fragments or variants
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                                                                    the presence of
for each of the
         inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO:77
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                                                                                              gene
the
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27 - AUG - 2002 ABG64060

(first

entry)

Human albumin fusion protein #735.

Albumin fusion protein; therapeutic protein X; human albumin; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder;

ABG64060 RESULT 11

ABG64060 standard;

Protein;

444

A

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Qy
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              healing and epithelial cell profiferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunoasorbent assay (ELISA). The present sequence represents a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound the protein of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 allergies, neurological disorders (e.g., Alzheimer's disease Parkinson's disease), cognitive disorders, schizophrenia, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secreted protein of
   391
                                                                771
                                                                                                                                 335
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                                                                                                                                                                                                                                                                                                                                                                                             274
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                                                                                                                                                                      NVVCRVGFQRMYSTPCDPKYGAGIYFTKNLKNLAEK--AKKISAADKLIYVFEAEVLTGF
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                                                         FCQGHPLNTVPPPLSP-GAIDGHDSVVDNVSSPETFVIFSGMQAIPQYLWTCT
                                                                                                                                                                                                                                                                                                                         KKQFEKCGLQVLKVEKIDNEVLMAAFQRKKKMMEEKLHRQPVSHRLF-----QQVPYQFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNIEDMLCKVQEEMARKKERGLWRSLGQWTIQQQKTQDEMKENIIFLKCPVPPTQELLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSLONHHITENNHILYLGRKEHDILSQLQKTSSVSITEIISPGRTELEIEGARADLIEVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRKYTSVSLPAIGTGNAGKNPITVADNIIDAIVDFSSQHSTPSLKTVKVVIFQP--ELLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQNITSISFPALGTGNMEIKKETAAEILFDEVLTFAKDHVKHQL-TVKFVIFPTDLEIYK
FTKGRAGLVTPPPKNPHNPTDLFDSVTNNTRSPKLFVVFFDNQAYPEYLITFT
                                                                                                                          -- VNQHGFNRSCAGKNAVSYGKGTYFAVDASYSAKDTYSKPDSNGRKHMYV--VRVLTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----HWTDMNHQLF----CMVQLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 26.11; Conservative
                                                                                                                                                                                                                                                            -----KIERIQNAFLWQSYQVKKRQMDIKNDHKNNERLLFHGTDADSVPY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.2%;
26.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 363; DB
Pred. No. 6e-2:
62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             RTCSSYAIE --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----PGQSEYN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     schizophrenia, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -FSMTTCNLPE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 444;
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443
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Best Local
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldr-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthitis). ABG63326-ABG65518 represent albumin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-2000;
25-APR-2000;
21-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiinleer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            fusion proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                  52
                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
MNIEDMLCKVQEEMARKKERGLWRSLGQWTIQQQKTQDEMKENIIFLKCPVPPTQELLDQ 657
                                                                                                                                                                                                                             AVESE-CAVLAAQPHRD--FIITPGGCLKCKIIIHV-----PGGKDVRKTVTSVLEECE 162
                                                                                                                                AFSSEMAKRSKMLSLNNYSVPQSTREEKRENGLEARSPAINLMGFNVEEMYEAHAWIQRI
                                                                                                                                                                                                                                                   EMKSEFLATKAKQFQRSQLVLVTKGFNLFCKYIYHVLWHSEFPKPQILKHAMKECLEKCI 418
                                                                                                                                                                                                                                                                                               VGTVSKPCFTAYEMKIGAITFQVATGDIATEQVDVIVNSTXRTXNXXSGXSRAILEGAGQ 111
                                                                LSLQNHHIIENNHILYLGRKEHDILSQLQKTSSVSITEIISPGRTELEIEGARADLIEVV 597
                                                                                                                                                                                              EQNITSISFPALGTGNMEIKKETAAEILFDEVLTFAKDHVKHQL-TVKFVIFPTDLEIYK 477
                                                                                                IFYDSMKKRDLSASLNF----QST-----
                                                                                                                                                                QRKYTSVSLPAIGTGNAGKNPITVADNIIDAIVDFSSQHSTPSLKTVKVVIFQP--ELLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page
                                                                                                                                                                                                                                                                                                                                                                                                                               444 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2000US-229358P.
; 2000US-199384P.
; 2000US-256931P.
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US11988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for treating disease
                                                                                                                                                                                                                                                                                                                                                                              8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2102pp;
                                 ---CMVQLE----
                                                                                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                                                                                                                                                                                            Score 363; DB 23;
Pred. No. 6e-22;
2; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
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                                 ----PGQSEYN---
                                                                                                  -FSMTTCNLPE-
                                                                                                                                                                                                                                                                                                                                                               178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diabetes comprises
                                                                                                                                                                                                                                                                                                                                                                                            Length 444;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB84807
                                        holoenzyme delta subunit proteins and agents that modulate their activity. The agents are useful in the treatment of bacterial infections e.g. S. pyogenes, S. aureus, S. pneumoniae, Mycoplasma, Yersinia, Corynebacterium, Salmonella, Mycobacterium tuberculosis or M. leprae. The invention provides a convenient means of identifying compounds which modulate DNA replication in bacteria and therefore provide antibacterial targets, and which are also useful for amplification of DNA. ABL87935 to ABL88071 and ABB84724 to ABB84816 represent sequences used in the exemplification of the present
Sequence
                                                                                                                                                                                 The present invention describes nucleic acid sequences encoding a DNA polymerase III holoenzyme delta subunit (I) from bacteria. (I) has antibacterial; tuberculostatic; antileprotic. Methods from the present invention can be used for screening for bacterial DNA polymerase
                                                                                                                                                                                                                                                              Example
                                                                                                                                                                                                                                                                                           Nucleic acid encoding a DNA polymerase III holoenzyme delta subunit from bacteria, useful for screening agents that modulate the subunit activity which is useful in the treatment of bacterial infections e.g. S. pyogenes and S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                       Bullard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUL-2000;
28-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB84807 standard; Protein; 599 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REPL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200206532-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacterial infection; DNA replication modulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- VNQHGFNRSCAGKNAVSYGKGTYFAVDASYSAKDTYSKPDSNGRKHMYV--VRVLTGV 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKQFEKCGLQVLKVEKIDNEVLMAAFQRKKKMMEEKLHRQPVSHRLF-----QQVPYQFC 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -TIKDKET-
                                                                                                                                                                                                                                                                 12;
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599
                                                                                                                                                                                                                                                            Page 84; 500pp; English.
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2001US-0818780.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001WO-US22395
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AA;
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Query Match Best Local

Similarity

6.6%; 31.9%;

Score Pred.

291.5; DB 23; No. 1.1e-15;

Length 599;

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Вb
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                                                                                                                                                                                                                                                                                                                                 27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                     The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-off primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein
                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB94051;
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                                                                                                                                                Claim
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                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-2000; 2000EP-0116126
 polynucleotide which
             sequence and an oligonucleotide comprising a sequence complementary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIQEESDRIVQERGRVPTGEAVVTSAGKLKAKYVIHTVGPVW----RGGSHGEDELLYKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIQEESKQFVARYGKVSAGEIAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTGKLQRAIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYGGESMAEVRKELEYKGKKIRIVKGDITREEVDAIVNAANEYLKHGGGVAGAIVRAGGS
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                                                                                                                                                                                                                                                                 Isogai T,
3, Sugiyama
                                                                                                                                             SEQ ID 14218; 2537pp + CD ROM;
                                                                                                                                                                                                                                                                                                                               99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                      99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289
                                                                                                                                                                                                                                                                 Nishikawa T,
T, Wakamats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
 comprises a
                                                                                                                                                                                                                                                                    Wakamatsu
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 3'-end
                                                                                                                                                                                                                                                               Hayashi K, S
A, Nagai K,
 sequence,
                                                                                                                                             English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91;
                                                                                                                                                                                                                                                                              Saito K,
                                                                                                                                                                                                                                                                    Otsuki
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 where the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
 361
                                   766
                                                                        306
                                                                                                              706
                                                                                                                                                   246
                                                                                                                                                                                       660
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                                                                                                                                                                                                                                                              617
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VLTGIYTHGNHSLIVPPSKNPQNPTDLYDTVTDNVHHPSLFVAFYDYQAYPEYLIT 416
                                                                                                                                                                                                                                                                                                                                                                      TEKEQCPYTSEDECTKDFDEKEYQELNELQKKLNINIS--LDHKRPLIKVLGISRDVMQA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEMAKRSKMLSLNNYSVPOSTREEKRENGLEAR--SPAINLMGENVEEMYEAHAWIORI 537
                                 VLTGFFCQGHPLNIVPPPLSP-GAIDGHDSVVDNVSSPETFVIFSGMQAIPQYLWT 820
                                                                        SVPH----
                                                                                                            QVPYQFCNVVCRVGFQRMYSTPCDPKYGAGIYFTKNLKNLAEKAKKISAADKLIYVFEAE
                                                                                                                                                                                                                                                                                                 RDETEAMIKRVRLAKEQESRADCISEFIEWQYNDNNTSHCFNKMTNLKLEDARREKKKTV
                                                                                                                                                                                                                                                                                                                                                                                                             LSL-QNHHIIENNHILYLGRKEHDILSQLQKTSSVSITEIISPGRTELEIEGARADLIEV 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSQQSVMSKLASFLGFS--KQSPQKKNHLVLEKKTESATFRVCGENVTCVEYAISWLQDL
                                                                                                                                               EYNTVASKFNQTCSHFRIEKIERIQNPDLWNSYQAKKKTMDAKNGQTMNEKQLFHGTDAG
                                                                                                                                                                                       QF-----
                                                                                                                                                                                                                        DVKINHRHYTVNLNTYTATDTKGHSLSVQRLTKSKVDIPAHWSDMKQQNFCVVELLPSDP
                                                                                                                                                                                                                                                              -----RGLWRSLGQWTIQQQKTQDEMKENIIFLKCPVPP---
                                                                                                                                                                                                                                                                                                                                      VMNIEDMLCKVQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                        -VNRNGFNRSYAGKNAVAYGKGTYFAVNANYSANDTYSRPDANGRKHVYYVR
                                                                                                                                                                                     -EKCG-LQVLKVEKIDNEVLMAAFQRKKKMMEEKLHRQPVSHRLFQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 256; DB 22;
Pred. No. 6.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                              ---TQELLDQKK
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                                                                                                              765
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RESULT 14
ABB49353
                                                                                       Antibacterial; vitamin B12; b
                                                                                                                                                   ABB49353 standard;
                                                                                                          Listeria monocytogenes protein #2057
                                                                                                                         05-FEB-2002
                                                                                                                                        ABB49353;
                                              18-OCT-2001
                                                            30200177335-A2
                                                                         Listeria monocytogenes
                                                                                      l; gene therapy; vaccine; biosynthesis;
bacterial infection; disease.
                                                                                                                        (first entry)
                                                                                                                                                    Protein;
                                                                                                                                                    176
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biodegradation;

11-APR-2001;

2001WO-FR01118

(INSP ) INST PASTEUR

11-APR-2000; 2000FR-0004629

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RESULT 15
AAU58306
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by leading the proteins and the treatment or prevention of infections by leading to the treatment or prevention of infections by leading to the treatment or prevention of infections by leading to the prevention of the treatment or prevention of the treatment or prevention of the prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, are for biosynthesis and biodegradation, especially biosynthesis of Vitamin and Telephone sequence are useful for the second of Vitamin and Telephone sequence of the sequence and related organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Danies Garage Chakraborty T, Domann Chakraborty T, Domann Perez-Diaz J, Baquero
                                                                                                                                 SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteom, uveitis; endophthalmitis; bone; joint; central nervous system; finflammatory lesion; acne vulgaris; enzyme linked immunosorbent
WO200181581-A2
                                                                                                                                                                                            SAPHO syndrome; synovitis;
                                                                                                                                                                                                                                                    Propionibacterium acnes immunogenic protein
                                                                                                                                                                                                                                                                                                                                                                                                                         AAU58306 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic sequence for Listeria monocytogenes, useful {\tt e.g.} for and prevention of Listeria and related bacterial infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chakraborty T, Domann E, Perez-Diaz J, Baquero F, Maduenio E, De Pablos B,
                                                    Propionibacterium
                                                                                                            dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 monocytogenes and related organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        te: The sequence data for this patent did not ecification, but was obtained in electronic for ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NISTGVYGFPKKLAAEVALYTVRKWAE-EEYDTSIKEIRFVCFDEENLKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALSSGIFQFPLNLCTKTIVETIRVSLQGKPMMSNLKEIHLVSNEDPTVAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEAVITSAGDLKATYIIHAVGPIWKDGEHQE-ANKLASCYWKALDLAAGKD--LTSIAFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IELSVWKDDLTTHAVDAVVNAANEDLLHGGGLALALVKAGGFEIQEESKQFVARYGKVSA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEIAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTGKLQRAIVSILNYVIYKNTHIKTVAIP 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AΑ;
                                                                                                         osteopathic;
                                                                                                                                                                                                                                                                                                            entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                         246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 235; DB 23;
Pred. No. 1.1e-11;
9; Mismatches 73
                                                                                                         neuroprotectant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaerst U,
                                                                                                                                                                                                                                                       #19202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   part of the
                                                                                                                                                                                            osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The acnes proteins may also be used as diagnostic agents for determining P. acnes presence for example by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences AAU39105-AAU68017 represent Propionibacterium acnes
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 QT-----VTKVDTIYLVAFNAEAEAGYRAA
                                                                                                                                           AGGGGVDGAIHRAAGPELSQACRKLRETTLTDGLPTGQSVATTAGKMPAKWVIHTVGPVW
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                                 VSLQGKPMMSNLKEIHLVSNEDPTVAAFKAASEFILGKSELGQE: 304
                                                                       AKTIDKSDQLASCYRTSLHVADEI-----GARTIAFPTISAGVYGYPMDEATRIAVETCR
                                                                                                                                                                                                                 LLANSRASIAVTPDDSAEGDRGSCTI-----GAMADITILRADITTLDVDAVVNAANRQL
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, Jen S, Carter
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Pred. No. 4.1e-10;
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US-08-826-267-2

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                                   Query Match
Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows CURRENT APPLICATION DATA:
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OPERATING SYSTEM:
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CLONE: 205276
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                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
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US-09-723-262-2
US-09-723-219-2
US-09-723-219-2
US-09-723-219-2
US-08-960-022-14
US-08-844-058-2
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Sequence 14, Appli
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Post-processing: Minimum Match

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Best Local Similarity
                 Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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                                                                                 IMMEDIATE SOURCE:
LIBRARY: GenBa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 LVKAGGFEIQEESKQFVARYGKVSAGEIAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTGK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 GAPTDGFTVLSTKSLFLGQK------LQVVQADIASIDSDAVVHPTNTDFYIGGEVGST 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 KLEAIITPPPAKKAKSPSQKKPVAKKTGG--KKGARK-----SKKQGEVSKAASADSTTE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55
                                                                      CLONE:
                                                                                                                    TOPOLOGY:
                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/353,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL-----GENYSWQIPINHNDFKILKNNERQLCEVLQNKFGCISTLVS--PVQE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAGAAAYNEKSGRITSLSLLFQKVFAQIFPQWRKGNT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
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                                                                 7: GenBank
205276
                                                                                                                                                      amino acid
                                                                                                                                                                    368 amino acids
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3174 Porter Drive
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                                                                                                                                                                                                                           415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: DOS
FastSEQ for Windows Version
                                                                                                                      linear
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 3.7%;
24.1%;
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                                                                                                                                                                                                                                                                            PF-0255 US
Score 165.5; DB 4;
Pred. No. 8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inc
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              Length 368;
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                                                                                                                                           INFORMATION FOR SEQ ID NO:
IMMEDIATE SOURCE:
LIBRARY: BRSTN
CLONE: 2297753
                                                                                                                                                                              TELEPHONE: 415-855-0555
                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 KLEAIITPPPAKKAKSPSQKKPVAKKTGG--KKGARK----SKKQGEVSKAASADSTTE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 LEKKGGKEFVEAVLELRKKNGPLEVAGAAVSAGHGLPAKFVIHCNSP---VWGSDKCEEL 285
                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM CO
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3174 Por CITY: Palo Alto
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                                                      TOPOLOGY:
                                                                     STRANDEDNESS:
                                                                                          TYPE:
                                                                                                                                                              TELEFAX:
                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version
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                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76;
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                                                                                                   373 amino acids
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                                                                                                                                                              415-845-4166
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                   BRSTNOT 05
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                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                       US/08/824,878
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RESULT 4
US-09-353-688-1
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Patent No. 6136314
GENERAL INFORMATION:
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Best Local :
                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                      TOPOLOGY: line
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 KLEATITPPPAKKAKSPSQKKPVSK-----KAGGKKGARKSKKKQGEVSKAASADSNNR 176
                                                                                                                                                                                                                                     NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
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  LIBRARY: BRSTNOT05
CLONE: 2297753
                                                                             STRANDEDNESS:
                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALVKAGGFEIQEESKQFVARYGKVSAGEIAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTG 211
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                                                                                                                                                                                                                                       PF-0255 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09722139 Patent No. 6355471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 1055
CURRENT APPLICATION NUMBER: US/09/722,139
CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Freedman, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1375
TYPE: PRT
                      213
                                                                                                                                                                            114
                                                                                                 166
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                                                                                                                                                                                                                110 YTMMGNSGDSGLIP----RICEGLFSRINETTRWDEASFRTEVSYLEIYNERVRDLLRRK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 IKTVYFVLFDSESIGIY 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 LKEIHLVSNEDPTVAAF 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 KLQRAIVSILNYVIYKNTHIKTVAIPALSSGIFQFPLNLCTKTIVETIRVSLQGKPMMSN 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 TLEKKGGKEFVEAVLELRKKNGPLEVAGAAVSAGHGLPAKFVIHCNSP---VWGADKCEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 ALVKAGGFEIQEESKQFVARYGKVSAGEIAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 GEHLPDGFTVLSTKSLFLGQKLNLIHSEIS----NLAGFEVEAIINPTNADIDLKDDLGN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 KLEAIITPPPAKKAKSPSQKKPVSK-----KAGGKKGARKSKKKQGEVSKAASADSNNR 176
                                                                                                                                                                                                                                                         62 WQIPINHNDFKILKNNERQLCEVLQNKF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 ---VQEG----NSKSLQVFRKMLTPRIELSVWKDDLTTHAVDAVVNAANEDLLHGGGLAL
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                                                                                                                                                                                                                                                                                            59 DFSFYSA----DTKSPDYVSQEMVFKTLGTDVVKSAFEGYNACVFAY-----GQTGSGKS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                            2 DESMVAGAAAYNEKSGRITSLSLLFQKVFAQIFPQWRKGNTEECLPYKCSETGALGENYS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 VAGAAAYNEKSGRITSLSLLFQKVFAQIFPQWRKGNT------
                      LQRAIV
                                                                                               KQFVARYGKVSAGEIAVTGA---GRLPCKQI--IHAVGPRWME-WDKQGCT------GK 212
                                                                                                                                                                            LTPRIELSV---
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                                                                                                                                     SSKTFNLRVREHPKEGPYVEDLSKHLVQNYGDV--EELMDAGNINRTTAATGMNDVSSRS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
72; Conser
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                                                                                                                                                                          -----WKDDLTTHAVDAVVNAANEDLLHGGGLALALVKAGGFEIQEES 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Richard No. 635547lel motor proteins and methods
                                                          · IKFTQAKFDSEMPCETVSKIHLVDLAGSERADATGATGVRLKEGGN
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18.7%;
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22.7%; Pred. No. 3.
-SILNYVIYRNT--HIKTVAIPALSSGIFQFPLNLCT---
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                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.00
l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Score 136.5; DB Pred. No. 0.0033
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1; Mismatches
                                                                                                                                                                                                                                                     ----GCISTLVSPVQEGNSKSLQVFRKM 113
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.3e-06;
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                                                                                                                                                                                                                                                                                                                                                                         Indels 239;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 1375;
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Gaps

38;

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Sequence 2, Application US/09721832
Patent No. 6399346
GENERAL INFORMATION:
APPLICANY: Beraud, Christophe
APPLICANY: Freedman, Richard
TITLE OF INVENTION: No. 6399346el motor proteins and
TITLE OF INVENTION: their use
FILE REFERENCE: 1055
CURRENT APPLICATION NUMBER: US/09/721,832
CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Human
US-09-721-832-2
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US-09-721-832-2
                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
LENGTH: 1375
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
  114 LTPRIELSV-------WKDDLTTHAVDAVVNAANEDLLHGGGLALALVKAGGFEIQEES 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           535
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                                                                       110 YTMMGNSGDSGLIP----RICEGLESRINETTRWDEASFRTEVSYLEIYNERVRDLLRRK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             509
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                                                                                                                                                                    59
                                                                                                                                                                                                                                                            Local Similarity
nes 154; Conserv
                                                                                                                                                                                                          2 DFSMVAGAAAYNEKSGRITSLSLLFQKVFAQIFPQWRKGNTEECLPYKCSETGALGENYS
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                                                                                                                  WQIPINHNDFKILKNNERQLCEVLQNKF------GCISTLVSPVQEGNSKSLQVFRKM 113
                                                                                                                                                               DFSFYSA----DTKSPDYVSQEMVFKTLGTDVVKSAFEGYNACVFAY-----GQTGSGKS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEKE-----QVMLVAHLEEQL-----REKQEMIQLLRRGEV 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKKQFEKCGLQVLKVEKIDNEVLMAAFQRKKKMMEEKLHRQPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NHPKE------AAKLREKRKSGLLSSFSLSMTDLSKSRENLSAVMLY 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHVKHQLTVKFVIFPTDLEIYKAFSSEMAKRSKMLSLNNYSVPQSTREEKREN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARVQELTKEWTNKWNETQNILKEQTLALRKEGI-----GVVLDSELPHLI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETFLRVQEELQRLKELNNNEKAEKFQIFQELDQLQKEKDEQYAKLELEK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPGLEFERQQREELEKLESKRKLIEEMEEKQKSDKAELERMQQEVETQRKETEIVQLQIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGK-SELGQETTPSFNAM--VVNNLTLQIVQGHIEWQTADVIVNSVNPHDITVGPVAKSI 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANRAKNIINKPTINEDANVKLIRELRAEIARLKTLLAQGNQIALLDSPTALSMEEKLQQN 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INKSLVTLGAKKKQVFVPYRDSVLTWLLKDSLGGNSKTIMIATISPADVNYGETLSTLRY
                                                                                                                                                                                                                                                            Conservative 131;
                                                                                                                                                                                                                                                                                 3.1%;
18.7%;
                                                                                                                                                                                                                                                         Score 136.5; DB Pred. No. 0.0033 1; Mismatches 2
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                       Ω
                                                                                                                                                               ; ORGANISM: Human US-09-721-689-2
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US-09-721-689-2
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CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
                                                                Query Match 3.1%; Score 136.5; DB Best Local Similarity 18.7%; Pred. No. 0.0033; Matches 154; Conservative 131; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09721689 Patent No. 6440685
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Freedman, Richard TITLE OF INVENTION: No. 6440685el motor proteins TITLE OF INVENTION: their use FILE REFERENCE: 1055
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                                                                                                                                                                                                          LENGTH: 13
TYPE: PRT
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                                            SOFTWARE:
SEQ ID NO 5
                                                                  CURRENT APPLICATION NUMBER: US/09/350,982C
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
                                                                                                                                                                       TITLE OF INVENTION: Tank
                                                                                                                                                     FILE REFERENCE:
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                                                                                                                                                                                                                 Isacchi, Antonella
                                                                                                                                                                                                                                       Toma, Salvatore
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US-08-973-462-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-350-982C-5
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OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (1102)...(1102)
OTHER INFORMATION: n is any nucleic acid
NAME/KEY: misc_feature
LOCATION: (2650)...(2650)
OTHER INFORMATION: n is any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08973462B Patent No. 6191270
                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/973,462B CURRENT FILING DATE: 1998-02-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC
FILE REFERENCE: 0660-0125-0 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: 1995-06-13 NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1996-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: FR 95/07007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1786
                                                                                                                                                                                                                                                              845
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les 43; Conserv
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                                            VSLQGKPM---
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                                                                                                                                                                                                                                                           LNEIEEVKENVVTTILENVEETTAESVTTFSNILE----EIQENTITNDTIEEKL----
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                                                                                                                            WMEWDKQGCTGKLQRAIVSILNYVIYKNTHIKTVAIPALSSGIFQFPLNLCTKTIVETIR
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                                                                                      --EQAEEKSANTITEIFENLEENAVESNENV-AENLEKLNETVFNTVLDKVEET-VEISG
                                                                                                                                                                         - EELHENVLSAALENT - - - QSEEEKKEVIDVIEEVKE - EVATT - - - - - - - - LIETV - - -
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                                                                                                                                                                                                                                                                                                                                                124;
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                                        ----MSNLKEIHLVSNEDPTVAAFKAASEFILGKSELGQETTPSFNAM 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIERRE
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Pred. No. 0:011;
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Pred. No. 0.0043;
8; Mismatches 7;
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-QENLLTGMFRSIETSIVIQSEEKVDLNENVVSS
                                                                                                                                                                                                                                                                                                                                                264;
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US-08-801-263A-9
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                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                               SEQUENCE CHARACTERISTICS:
LENGTH: 2512 amino aci
                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 919-420-2200
                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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CTTY: Charlotte
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                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                        NAME: Sibley, Kenneth D. REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 VVNNLTLQIVQGHIEWQTADVIVNSVNPHDITVG---PVAKSILQQAGVE-----MKSEF
TOPOLOGY:
                                                                                      TELEFAX:
                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 19-FEE
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                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                  amino acid
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                               2512 amino acids
                                                                                      919-881-3175
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VENTION: System for the In Vivo Delivery and VENTION: Expression of Heterologous Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Davis, Nancy L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnston, Robert E.
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bell Seltzer Park & Gibson,
                                                                                                                                                                                                                                                                                                                                                                                                           5811407th Carolina
                                                                                                                                                                                                                                                                                                                                    Floppy disk
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                                                                                                                                                                                                                                                                                  Version
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RESULT 11
US-09-102-248-9
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                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson,
STREET: 1211 East Morehead Street
                    SEQUENCE CHARACTERISTICS
                                                                    TELEPHONE: 919-420-2200
                                                                                                                                                    FILING DATE: 19-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Davis, Nancy L. APPLICANT: Simpson, Dennis A.
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                                    TELEPHONE: 919-881-3175
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                                                                                                   NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1211 East Morehead St
CITY: Charlotte
STATE: No. 6008035th Carolina
                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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   LENGTH:
                                                                                                                                                                                                                                           FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --NEHNIKSVAIPLLSTGIYAAGKDRLEVSLNCLTTALDRTDADVTIYCLDKKWKERIDA 1501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --RWPTSFTDSATETGTARMTVCLGKKVIHAVGPDFRKHPEAEALKLLQNAYHAVADLV- 1443
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                                                                                                                                                                                                                                                                                                                                                                             28234
                                                                                                                                    Sibley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09102248
2512 amino acids
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                                                                                                                                                                                                                                                                                                   3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           System for the In Vivo Delivery and Expression of Heterologous Genes in
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                                                                                                                                                                                       SD
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Pred. No. 0.021;
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Best Local :
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                                  INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1444 -- NEHNIKSVAIPLLSTGIYAAGKDRLEVSLNCLTTALDRTDADVTIYCLDKKWKERIDA 150:
 SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino aci
                                                                                       TELECOMMUNICATION INFORMATION TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                 FILING DATE: June 10, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169
                                           TELEFAX: 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77
                                                                                                                          NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
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                                                                                                                                                                                                    APPLICATION NUMBER: 0: FILING DATE: June 10,
                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                      201-343-1684
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Smith, Susan
amino acids
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Pred No. 0.021;
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US-08-801-263A-5
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                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                            SOFTWAKE: CULTION DATA:
CURRENT APPLICATION DATA:
US/08/801,263A
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MEDIUM TYPE: Floppy disk
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                SEQUENCE CHARACTERISTICS:
                                                                          TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1041 EH--LRDIFETEQITLDVLADMGHEELKEIGINAYGHRHKLIKGVERLL-------GG
                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                        NAME: Sibley, Kenneth D. REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                       FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                              COUNTRY:
                                              TELEFAX:
                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKCG-----LQVLKVEKIDNEVLMAAFQRKKKMMEEKLHRQPVSHRLFQQVPYQFCNVVC 716
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                                                                                                                                                                                                                                                                                                                      Charlotte
No. 5811407th Carolina
                                                                                                                                                                                                                                                                                                 28234
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                                             919-881-3175
                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davis, Nancy L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simpson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnston, Robert E.
                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
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amino acids
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System for the In Vivo Delivery and
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Pred. No. 0.0081;
                                                                                            5470-147
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Best Local S
Matches 123
                                                                                                                                                                                                                                                             Sequence 5, Application US/09102248 Patent No. 6008035
                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Davis, Nancy L.
APPLICANT: Simpson, Dennis A.
TITLE OF INVENTION: System for the In Vivo Delivery and
TITLE OF INVENTION: Expression of Heterologous Genes in
NUMBER OF SEQUENCES: 12
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                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson,
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COMPUTER READABLE FORM
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                                                               STREET: 1211 Has CITY: Charlotte
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                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                     SEGSLFSSFSGSDNSITSMDSWSSGPSSLEIV 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                        RKYIEAPEQPAAPPAQAEEAPEVAATPTPPAADNTSLDVTD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPVAKSILQQAGVEMKSEFLATKAKQFQRSQLVLVTKGFNLFCKYIYHVLWHSE-----
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Matches 123; Conservative
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ATTORNEY AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 919-420-2200
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APPLICATION NUMBER: US 0
FILING DATE: 19-FEB-1997
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SEGSLESSESGSDNSITSMDSWSSGPSSLEIV 1750
                                                                                                                                                                                                                                                                      ----FPKPQ-----ILKHAMKECLEKC-IEQNITSI---SFPALGTGNMEIKKETA 442
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                                                                                                                                                                                                                                  IKVLFPNDQESNEQLCAYILGETMEAIREKCPVDHNPSSSPPKTLPCLCMYAMTPER---
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                                                                              RKYIEAPEQPAAPPAQAEEAPEVAATPTPPAADNTSLDVTD-
                                                                                                                                                                                            AEILFDEVLTFAKDHVKHQLTVKFVIFPTDLEIYKAFSSEMAKRSKMLSLNNY-----
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                                        IENNHILYLGRKEHDILSQLQKTSSVSITEII 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 131; DB 3; Length 2517; Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatchés 216;
                                                                                                                                                                                                                                                                                                            -----SYFEGTKFHQAAKDMAE 1563
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                                                                            -ISLDMEDS 1718
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US-08-468-57<u>6</u>B-17
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 109; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tent No.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08
FILING DATE: O6-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 05-MAY-1994
PRIOR APPLICATION DATA:
                                  201 NYYKREIEEQLRAEMCQKLKFFKDTEIAKIKMEAKKKYEKELTMFQNDFEKACQ-----
                                                                     346 GPVAKSILQQAGVEM--KSEF-----LATKAKQFQRSQLVLVTKGFNLFCKYIYHVL 395
                                                                                                          147 LAEYHQAKESCNMETQTSSTFNRDSLAEKLQL-----IDDQFADAYPQRIKFESLEIKL 200
                                                                                                                                              291 ASEFILGKSELGQETTPS--FNA-MVVNNLTLQIVQGHIEWQTADVIVNSV--NPHDITV 345
                                                                                                                                                                                                                     240 SSGIFQFPLNLCTKTIVETIRVSLQ---GKPMMSNLKEIHLVSNEDP-----TVAAFKA 290
396 WHSEFPKPQILKHAMKECLEKCIEQNITSISFPALGTGNMEIKKETAAEILFDEVLTFAK 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                               90 SLSVF-FPESGLAKEKVFTMQDLLQLIKINPTSSLYKS--LVSGSDKENQKGFLMHFLKE 146
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IOR APPLICATION DATA:
APPLICATION NUMBER: US 07/715,181
FILING DATE: 14-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 17-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10591-5144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Sprung Kramer Schaefer & Briscoe
660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                            2.9%; Score 130.5; ilarity 21.9%; Pred. No. 0.0 Conservative 80; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rabin, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       System 7.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 07/441,703
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                                                                                                                                                                                                                                                            194;
                                                                                                                                                                                                                                                                                             Length 712;
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Db 498 EEFESCRQALHKQLQDEI 515
QY 677 EVLMAAFQRKKKMMEEKL 694
Db 443 EKL-ELLAQNKLLKQQLEESRNENLRLLNRLAQPAPELAVFQKELRKAEKAIVVEH 497
Qy 617 RGLWRSLGQWTIQQQKTQDEMKENIIFLKCPVPPTQELLDQKKQFEKCGLQVLKVEKIDN 676
Db 389 INSKKEELNQSVNRVKELELELESVKAQSLATTKQNHMLNEKVKEMSDYSLLKE 442
Qy 568TSSVS-ITEIISPGRTELEIEGARADLIEVVMNIEDMLCKVQEEMARKKE 616
Db 331 QEQNIKSFEETYDRKLKNELLKYQLELKDDYIIRTNRLIEDERKNKEKAVHLQEELIA 388
Qy 515 PAINLMGFNVEEMYEAHAWIQRILSLQNHHIIENNHILYLGRKEHDILSQLQK 567
Db 283 -YAQRQLLLKDMDLLRGREAELKQRVEAFELNQKLQEEKMKSITEALRR 330
Qy 456 DHVKHQLTVKFVIFPTDLEIYKAFSSEMAKRSKMLSLNNYSVPQSTREEKRENGLEA-RS 514
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Search completed: May 1 • 2003, 11:46:17 Job time : 45 secs

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Scoring table:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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Gapop 10.0 , Gapext 0.5
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          /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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US-09-882-529-13

US-09-882-529-13

US-09-882-529-16

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US-09-882-529-16

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US-09-882-529-14
        US-09-731-001-5
US-09-731-001-2
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US-09-951-401-3	US-09-951-402-3	US-09-808-602-68	US-09-815-242-13228	US-09-893-519A-34	US-09-972-115A-4	US-09-972-115A-2	US-09-981-900B-9	US-09-727-384-6	US-10-023-219-4	US-09-801-574-76	US-09-764-846-236	US-10-091-483-236	US-09-815-242-5335	US-09-927-597-4	US-09-927-597-2	US-09-841-835-2	US-09-972-115A-8	US-09-742-096-3	US-09-509-196A-2	US-09-964-899-41	US-09-972-115A-6	US-10-102-806-517	US-09-991-258-3	US-09-815-242-12403	US-09-731-001-3
e ω		Sequence 68, Appl	Sequence 13228, A	34	4	Sequence 2, Appli	Sequence 9, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 76, Appl	Sequence 236, App	Sequence 236, App	Sequence 5335, Ap		Sequence 2, Appli	Sequence 2, Appli	œ	Sequence 3, Appli	Sequence 2, Appli	_	Sequence 6, Appli		Sequence 3, Appli	Sequence 12403, A	Sequence 3, Appli

## ALIGNMENTS

US-09-882-529-4

GENERAL INFORMATION:

Sequence 4, Application US/09882529 Patent No. US20020132317A1

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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 849; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Peyman, John A
APPLICANT: da Silva, Antonio
APPLICANT: Hockman, Paula
APPLICANT: Hockman, Paula
TITLE OF INVENTION: NOVEL INTERFERON-INDUCED TETRASPAN PROTEIN AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING SAME
FILE REFERENCE: 15966-771
CURRENT APPLICATION NUMBER: US/09/882,529
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/211,565
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GENERAL INFORMATION:

APPLICANT: Peyman, John A
APPLICANT: AB Silva, Antonio
APPLICANT: Hockman, Paula
TITLE OF INVENTION: NOVEL INTERPERON-INDUCED TETRASPAN PROTEIN AND
TITLE OF INVENTION: ACIDS ENCODING SAME
FILE REFERENCE: 15966-771
CURRENT APPLICATION NUMBER: US/09/882,529
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 609-212
PRIOR APPLICATION NUMBER: 609-212
PRIOR APPLICATION NUMBER: 609-211,565
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 819
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 Query Match
Best Local Similarity
Matches 815; Conserv
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                 Score 4208.5;
Pred. No. 0;
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GENERAL INFORMATION:

APPLICANT: Peyman, John A
APPLICANT: de Silva, Antonio
APPLICANT: Hockman, Paula
TITLE OF INVENTION: ACIDS ENCODING SAME
FILE REFERENCE: 15966-771
                                                                Sequence 3, Application US/09882529 Patent No. US20020132317A1
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                  TETRASPAN
                  PROTEIN
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CURRENT APPLICATION

NUMBER: US/09/882,529

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PRIOR FILING DATE: 2000-06-15

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH: 821

TYPE: PRT

ORGANISM: Homo sapiens
US-09-882-529-3
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Best Local Similarity
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                                                                                         LGQETTPSFNAMVVNNLTLQIVQGHIEWQTADVIVNSVNPHDITVGPVAKSILQQAGVEM 360
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FAQHPWRGFASGSPVD
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                                                    VPPPLSPGAIDGHDSVVDNVSSPETF-VIFSGMQAIPQYLWTCTQEYVQSQDYSSGPMRP
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Pred. No. 0;
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APPLICANT: Peyman, John A
APPLICANT: da Silva, Antonio
APPLICANT: Hockman, Paula
TITLE OF INVENTION: NOVEL INTERFERON-INDUCED TET
TITLE OF INVENTION: ACIDS ENCODING SAME
FILE REFERENCE: 15966-771
CURRENT APPLICATION UMBER: US/09/882,529
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/211,565
PRIOR APPLICATION NUMBER: 60/211,565
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US-09-882-529-7
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Best Local Similarity
Matches 178; Conserv
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                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/882,529
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/211,565
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: da Silva, Antonio
APPLICANT: Hockman, Paula
TITLE OF INVENTION: NOVEL INTERPERON-INDUCED
TITLE OF INVENTION: ACIDS ENCODING SAME
FILE REFERENCE: 15966-771
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NUMBER OF SEQ ID NOS: 16
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                                                              Score 841.5; DB 10;
Pred. No. 9.1e-59;
Pred. No. 9.1e-59;
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Pred. No. 2.7e-64;
1; Mismatches 0
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; ORGANISM: Homo sapiens US-09-882-529-15
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APPLICANT: Peyman, John A
APPLICANT: da Silva, Anto
APPLICANT: Hockman, Paula
                                                      SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 129
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/09882529 Patent No. US20020132317A1
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/882,529
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/211,565
PRIOR APPLICATION NUMBER: 60/211,565
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                      APPLICANT: Peyman, John A
APPLICANT: da Silva, Antonio
APPLICANT: Hockman, Paula
TITLE OF INVENTION: NOVEL INTERFERON-INDUCED TETRASPAN PROTEIN AND
TITLE OF INVENTION: ACIDS ENCODING SAME
FILE REFERENCE: 15966-771
                                                                                                                   PRIOR APPLICATION NUMBER: 60/211,565
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 16
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TYPE: PRT
ORGANISM: Homo sapiens
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US-09-882-529-11
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LENGTH: 121
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                                                                                                                                                                                                                                    Patent No. US20020132317A1
                                                                                                                                                                                                                                                      Sequence 13,
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                                                                                          APPLICANT: Peyman, John A
APPLICANT: da Silva, Antonio
APPLICANT: Hockman, Paula
TITLE OF INVENTION: NOVEL INTERFERON-INDUCED
TITLE OF INVENTION: ACIDS ENCODING SAME
FILE REFERENCE: 15966-771
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CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/211,565
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APPLICANT: da Silva, Antonio
APPLICANT: Hockman, Paula
                                                      CURRENT FILING DATE: 2001-09-12
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NUMBER OF
                PRIOR APPLICATION NUMBER: 60/211,565 PRIOR FILING DATE: 2000-06-15
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ORGANISM: Homo sapiens
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Pred. No. 6.1e-45;
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US-09-882-529-13
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                                                                              GENERAL INFORMATION:
                                                                                              Sequence 8, Application US/09882529 Patent No. US20020132317A1
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Best Local Similarity
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Best Local Similarity
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APPLICANT: da Silva, Antonio
APPLICANT: Hockman, Paula
TITLE OF INVENTION: NOVEL INTERFERON-INDUCED TETRASPAN PROTEIN AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING SAME
FILE REFERENCE: 15966-771
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CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/211,565
PRIOR FILING DATE: 2000-06-15
          APPLICANT: Peyman, John A
APPLICANT: da Silva, Antonio
APPLICANT: Hockman, Paula
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NUMBER OF SEQ ID NOS: 16
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ORGANISM: Homo sapiens
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ITLE OF INVENTION: NOVEL INTERFERON-INDUCED TETRASPAN PROTEIN AND NUCLEIC
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Best Local Similarity
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APPLICANT: HOOKman, Paula
TITLE OF INVENTION: NOVEL INTERFERON-INDUCED TETRASPAN PROTEIN AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING SAME
FILE REFERENCE: 15966-771
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CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/211,565
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 16
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CURRENT FILING DATE: 2001-09-12
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                                 240 SSGIFQFP 247
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                                                                                                         180 IAVTGAGRLPCKOIIHAVGPRWMEWDKOGCTGKLORAIVSILNYVIYKNTHIKTVAIPAL 239
                                                                      60 AVVTEGGNLPAKYVIHAVGPEASGYSKEGYE-LLENAYRACLRIAI--ELGIKSVAIPLI 116
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Pred. No. 1.2e
31; Mismatches
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Pred. No. 1.6e-09;
8; Mismatches 52;
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Best Local
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SEQ ID NO 12
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Best Local (
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Patent No. US20020132317A1
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/882,529
CURRENT FILLING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/211,565
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL INTERFERON-INDUCED TETRASPAN PROTEIN AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING SAME FILE REFERENCE: 15966-771
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CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/211,565
PRIOR FILING DATE: 2000-06-15.
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TITLE OF INVENTION: NOVEL INTERFERON-INDUCED TETRASPAN PROTEIN AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING SAME
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TYPE: PRT
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ORGANISM: Homo sapiens
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Local Similarity 41.4%;
nes 53; Conservation
58 AVGPNFSKGGEEEGDELLEKAYRAILR--LADENGIKSVAFPLLSTGIYGGPKDRAAQSL 115
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les 45; Conserv
                                                                                1 VNAANSRLLHGGGVAGAIARAAGKEAWPEA---FKKAPKCPVGEAVLTTGGGLPAKYVIH 57
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Hockman, Paula
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Search completed: May 13, 2003, 11:54:36 Job time: 59 secs
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; TYPE: PRT
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US-09-882-529-14
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APPLICANT: HOCKMAN, PAULA
TITLE OF INVENTION: NOVEL INTERFERON-INDUCED TETRASPAN PROTEIN AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING SAME
FILE REFERENCE: 15966-771
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centromere protein	chromosome segrega	myosin heavy chain	nonstructural poly	nucleotide-binding	RESA-H3 antigen PF	synaptonemal compl	PAM interacting pr	, PAM C-terminal int	myosin-3 heavy cha	hypothetical prote	genome polyprotein	nonstructural poly	nonstructural poly		T22I11.2 protein -

## ALIGNMENTS

conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Ju1-2000
C;Accession: B7:3568
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,

Hic

RESULT 1 B72368

A39403 conserved hypothetical protein [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text change 15-Jun-2001	ved hypothetical pies: Sulfolobus so: 24-May-2001 #sec	conser C;Spec C;Date	·
	2	RESULT	
IDEETTKIFE 594	584 NIDEETTKIFE 594	Db	
SNEDPTVAAFK 289	279 SNEDPTVAAFK 2	Оу	
525 VYNALLRAHELKLKSISMPAISTGIFGFPKERAVGIFSKAIRDFIDQHP-DTTLEEIRIC 583	525 VYNALLRAHELKLI	Db	
QFPLNLCTKTIVETIRVSLQGKPMMSN	220 ILNYVIYKN-THII	Qy	
VIQEESDRIVQERGRVPTGEAVVTSAGKLKAKYVIHTVGPVWRGGSHGEDELLYKA 524	469 VIQEESDRIVQER	Db	
EIQEESKQFVARYGKVSAGEIAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTGKLQRAIVS 219	160 EIQEESKQFVARY	QΥ	
KYGGESMAEVRKELEYKGKKIRIVKGDITREEVDAIVNAANEYLKHGGGVAGAIVRAGGS 468	409 KYGGESMAEVRKE	Db	
100 QEGNSKSLQVFRKMLTPRIELSVWKDDLTTHAVDAVVNAANEDLLHGGGLALALVKAGGF 159	100 QEGNSKSLQVFRKI	QУ	
359 GEGYLYPHDEGGEVKTNYLPEKLKNEVIFQPKRVGFEEELFERLRKLWPE 408	359 GEGYLYPHDFGO	Db	
57 GENYSWQIPINHNDFKILKNNERQLCEVLQNKFGCISTLVSPV 99	57 GENYSWQIPINHNI	Qy	
ch 6.6%; Score 291.5; DB 2; Length 599; l Similarity 31.9%; Pred. No. 1.8e-10; 80; Conservative 47; Mismatches 91; Indels 33; Gaps 7;	Query Match Best Local Similarity Matches 80; Conserv	Quer Best Matc	
A;Molecule type: DNA A;Residues: 1-599 <\armsolometarrow\armso	A;Molecule type: DNA A;Residues: 1-599 <arn> A;Cross-references: GB:A A;Experimental source: C;Genetics: C;Genetics: TM0508</arn>	A; Molecule A; Residues A; Cross-rei A; Experimen C; Genetics A; Gene: TM(	
Nature 399, 323-329, 1999 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316; PMID:10360571 A;Accession: B72368 A;Status: preliminary	Nature 399, 323-329, 199 A;Title: Evidence for 14 A;Reterence number: A72; A;Accession: B72368 A;Status: preliminary	Nature 399 A;Title: E A;Reference A;Accession A;Status:	
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C; Accession: A99469

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Science 294, 849-852, 2001

A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUID:21537279; PMID:11679669

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C;Superfamily: Pyrococcus abyssi hypothetical protein PAB0445
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                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain EGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-176 <GLA>
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A; Residues: 1-177 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A99139
A; Accession: A99469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: Sulfolobus solfataricus complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:NC_003210; PIDN:CAD00972.1; PID:g16412259; GSPDB:GN00177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE006641; NID:g13816268; PIDN:AAK43008.1; GSPDB:GN00155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: AF1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Listeria monocytogenes
Date: 27-Nov-2001 #sequence_revision
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                       118 NISTGVYGFPKKLAAEVALYTVRKWAE-EEYDTSIKEIRFVCFDEENLKLY
                                                                                                                                                 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 MPAISTGIYGYPFEICARIMANVLK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 GEIAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTG--KLQRAIVSILNYVIYKNTHIKTVA 235
                                                                238 ALSSGIFQFPLNLCTKTIVETIRVSLQGKPMMSNLKEIHLVSNEDPTVAAF 288
                                                                                                                                                                                                                            118 IELSVWKDDLTTHAVDAVVNAANEDLLHGGGLALALVKAGGFEIQEESKQFVARYGKVSA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 IELSVWKDDLTTHAVDAVVNAANEDLLHGGGLALALVKAGGFEIQEESKQFVARYGKVSA 177
                                                                                                        61
                                                                                                                                                                                                                                                                                            Local Similarity
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I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, I
R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
                                                                                                                                             GETAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTGKLQRAIVSILNYVIYKNTHIKTVAIP 237
                                                                                                                                                                                     MEITIVKGDITEQEVDVIVNAANSGLLGGGGVDGAIHQAAGPDLLKECQEVINRIGSCPA 60
                                                                                                    GEAVITSAGDLKATYIIHAVGPIWKDGEHQE-ANKLASCYWKALDLAAGKD--LTSIAFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPALSSGIFOFPLNLCTKTIVETIR 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEVAVTSAGKLKAKYVIHAVGPRY-----GIEGEDKLESAIFKSL--LKADELSLSSIA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEIYLIKGDITEIEADAIVNAANSYLQHGGGVAYAIVRKGGYIIQKESDEYVKKFGPVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59;
                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                          5.3%;
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                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Mismatches
                                                                                                                                                                                                                                                                                        Score 235; DB 2
Pred. No. 1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 288; DB 2;
Pred. No. 4.9e-11;
                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                       73;
                                                                                                                                                                                                                                                                                                           Length 176;
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Fsihi, H.
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A;Molecule type: DNA
A;Residues: 1-173 <RES>
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C; Superfamily: Pyrococcus
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A; Residues: 1-176 <GLA>
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R;Glaser, P.; Frangeul, L.;
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                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                           Similarity 57; Conserv
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55; Conserv
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27, 43-60, 1995
                                                                                                                                                                                                                            4.9%;
32.2%;
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eur. J. Biochem. 227, 43-60, 1995
A;Title: Metabolic pathway for biosynthesis of poly(3-hydroxybutyrate-co-4-hydroxybut
A;Reference number: 139561; MUID:95154322; PMID:7851418
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C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:L36817; NID:g695273; PIDN:AAC41426.1; PID:g695280 A;Experimental source: strain H16 / SK4040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Alcaligenes eutropnus
C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 23-Mar-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein 2 gbd-region [imported] - Alcaligenes eutrophus C:Species: Alcaligenes eutrophus
233 TVAIPALSSGIFQFPLNLCTKTIVETIRVSLQGKPMMSNLKEIHLVSNEDPTVAAFK
                                                                                                                                                                                                                                           120 LSVWKDDLTTHAVDAVVNAANEDLLHGGGLALALVKAGGFEIQEESKQFVARYGKVSAGE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 NISTGVYGFPKKLAAEVALYTVRKWAE-EEYDSSIKEVRFVCFDEENLTLY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 ALSSGIFQFPLNLCTKTIVETIRVSLQGKPMMSNLKEIHLVSNEDPTVAAF 288
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                                                                            AVITTGGHLPAPYVIHAVGPVWQGGD-QGEDELLANA-----YRNSIRLAAQHHLR
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                                                                                                                            IAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTGKLQRAIVSILNYVIYKNT------HIK 232
                                                                                                                                                                                        LQVVHGDITRMEVDAIVNAANSGLLGGGGVDGAIHGAGGSAIKEACRAIRDTQGGCPTGE 65
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                                                                                                                                                                                                                                                                                                                                                                                                         abyssi hypothetical protein PAB0445
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.ip11262
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                                                                                                                                                                                                                                                                                                                       Score 220; DB 2;
Pred. No. 8.5e-07;
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9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                 Length 173;
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surget, O.;
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Entian, K.
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Voss, H.; Wehla
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A;Cross-references: (C;Genetics: C;Gene: STY1184 C;Superfamily: Pyrocc
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A;Accession: E83182
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <STO>
A;Cross-references: GB:AE004789; GB:AE004091; NID:g9949857; PIDN:AAG07081.1; GSPDB:GN001
A;Experimental source: strain PA01
C;GenetLos:
A;Gene: PA3693
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB0445
                                                                                                                                                                                                                                                                       S:; Moule, S:; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C:; Quail, M.; Rutherford, K.;
A;Title: Complete genome sequence of a multiple
A;Reference number: AB0502; PMID:11677608
A;Accession: AD0636
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein STY1184 [imported] - Salmonella enterica subsp. C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 **sequence_revision 09-Nov-2001 **text_change 27-Nov-2001 C;Accession: AD0636 C;Accession: AD0636 C;Accession: AD0636 C;James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein PA3693 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 23-Mar-2001 C;Accession: E83182 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.
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                                          7, S.; Olson, M.V.
406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTGKLQ-RAIVSILNYVIYKNTHIKTVAIP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVRVWQGDITRLAVDAIVNAANSSLLGGGGVDGAIHRAAGAELVAACRLL---HG-CKTG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELSVWKDDLTTHAVDAVVNAANEDLLHGGGLALALVKAGGFEIQEESKQFVARYGKVSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AISCGIYGYPLEQAAAIAVEEV --- CRQRPAHSSLEEIVLVA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLAFPNISTGIYAFPRERAADIAIAAVREALAAAP---EIEQVTFVCFDDENYRLYR 169
                        VMTSR--LQVIQGDITQLSVDAIVNAANASLMGGGGVDGAIHRAAGPALLDACKLIRQQQ
                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                   Pyrococcus abyssi hypothetical protein PAB0445
                                                                                                Conservative
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                                                                                                                                                                                                                         GB:AL513382;
                                                                                                               4.6%;
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                                                                                                                                                                                                                       PIDN:CAD08271.1; PID:g16502318;
                                                                                         Score 204.5; DB 2;
Pred. No. 8.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 211; DB 2;
Pred. No. 3.1e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -RGGDNGEAELLASCYRRSLALAEQAGAASVAFP
                                                                                                                                                                                                                                                                                                                             ; Simmonds, M.; drug resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels.
                                                                                                                              Length 186;
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Dowd, L.; White, N.; Farrar
                                                                                                                                                                                                                                                                                                                           Skelton, J.; Stevens
Salmonella enterica
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                        64
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                                                                                                                                                                                                      submitted to the EMBL Data Library, A;Reference number: 221551
A;Accession maser:
                                                                                                                                                                                                                                                     C; Accession: T3
R: Seeger, K.J.;
                                                                                                                                                                                                                                                                                                                                                RESULT
T35937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: this accession replaces C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-190 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Date: 14-Au
C; Accession:
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                                                     A; Gene: SCOEDB
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                      Вþ
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                                                                                                             A; Experimental source:
                                                                                                                                                                                                    A; Accession: T35937
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Best Local
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   Local Similarity
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sion: E71027
                                                                          SCOEDB: SC9B5.17
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                                                                                                                                                                                                                                                                           T35937
                                                       Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                             strain
                                                                                                                                                                                                                                                                                                                                                                                                                      187
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 4.4%;
                                                                                                             A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
Score
Pred.
   No.
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A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: E71027
A;Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M.; Ohfuku, Y.; Fundaman....

DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the

A;Top-forence number: A71000; MUID:98344137; PMID:9879194
                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-169 <SEE>
A; Cross-references: EMBL: AL035206; PIDN: CAA22759.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: PH1513
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB0445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AP000006; NID:g3236133; PIDN:BAA30621.1; A;Experimental source: strain OT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.;
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SC9B5.17 - Streptomyces coelicolor C; Species: Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein PH1513 - Pyrococcus horikoshii C; Species: Pyrococcus horikoshii
                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 KDDLTTHAVDAVVNAANEDLLHGGGLALALVKAGGFEIQEE---SKQFVAR-YGK--VSA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEIAVTGAGRLP----CKQIIHAVGPR----WMEWDKQGCTGKLQRAIVSILNYVIYKNTH 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKVSAGETAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTGKLQRAIVSILNYVIYKNTHIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKSTAFPAISAGIYGCPLKEVVRTFKEVVKEFLK---VANHVKEVYLVLYSERD-----Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEVVVTPPMKLKENGVKYVIHTVGPYCGGVWSK-DKE---EKLKLAILGALKKA--DELG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IKTVAIPALSSGIFQFPLNLCTKTIVETIRVSLQGKPMMSNLKEIHLV--SNEDPTVAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGDITKFRAEAIVNAANKYLEHGGGVAYAIAKAASGDVSEYTRISKEEMRRQLGKDWIEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
                                                                       abyssi hypothetical
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                       January 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                               S.D.; Parkhill,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148
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                       194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1e-05;
ches 59;
; DB 2;
3.5e-05;
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                                                                       protein
                                                                                                                                                                               GSPDB:GN00070;
                                                                                                                                                                                                                                                                                                                                                          J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for a sequence replaced by
                     Length 169;
                                                                             PAB0445
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                                                                                                                                                                                                                                                                                                                                                               Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
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                                                                                                                                                                                                                                                                                                                                                            в.G.;
                                                                                                                                                                               SCOEDB:SC9B5.17
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                                                                                                                                                                                                                                                                                                                                                          Rajandream,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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hypothetical protein DKFZp434J214.1 - hum C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 23-Jul-1999 #sequence_revision 23 C;Accession: T12540 R;Wambutt, R.; Heubner, D.; Mewes, H.W.; submitted to the Protein Sequence Databas A;Reference number: Z17524 A;Accession: T12540 A;Status: preliminary
                                                                                        probable 1ppD protein - Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 C;Accession: H70517
             R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
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A;Experimental source: adult test
C;Genetics:
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 Nature 393, A; Authors:
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A; Residues: 1-359 <WAM>
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                                                                                                                                                                                                                                                                                                                                                                                                   EKYKRKKEYMNRKMFGRDRIINERHLFHGTSQDVVDGICKHNF------DPRVCGKHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSLGQWTIQQQKTQDEMKENIIFLKCPVPPTQELLDQKKQFEKCGLQVLKVEKIDNEVLM
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 Sgares,
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 J.E.;
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Pred. No. 0.00022;
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 Taylor,
                                                                                                              17-Jul-1998 #text_change 22-Oct-1999
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 Whitehead,
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 Barrell,
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RESULT C85666

probable polyprotein 21679

[imported]

Escherichia

coli (strain

O157:H7,

substrain

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C; Geneti
A; Gene:
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C; Superfamily:
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-J
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                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-177 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A; Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gasawara, N.; Yasunaga, DNA Res. 8, 11-22, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Hayashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-343 <COL>
A; Cross-references: GB:
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                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
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                                PALSSGIFQFPLNLCTKTIVETI 259
                                                                       TGHAVITLAGDLPAKAVVHTVGPVW-RGGEQNEDQLLQDAYLNSLRLVAANS--YTSVAF
                                                                                                                                              KTRIHVVQGDITKLAVDVIVNAANPSLMGGGGVDGAIHRAAGPALLDACLKVRQQQGDCP 61
                                                                                                                                                                               RIELSVWKDDLTTHAVDAVVNAANEDLLHGGGLALALVKAGGFEIQEESKQFVARYGKVS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVAIPALSSGIFQFPLNLCTKTIVETIRVSLQGKPMMSNLKEIHLVSNEDPTVAAFKAAS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IELEVHQADVTKLELDAITNAANTRLRHAGGVAAAIARAGGPELQRESTE----KAPIGL 229
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PAISTGVYGYPRAAAAEIAVKTV
                                                                                                          AGEIAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTGKLQRAIVSILNYVIYKNTHIKTVAI 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLALVAFGTGVGGFPLDDAARLMVGAVRRHRPG----SLQRVVFAVHGDAAERAFSAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T.; Makino, K.; Ohnishi,
N.; Yasunaga, T.; Kuhara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 29.(
56; Conservative
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32.2%;
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                                                                                                                                                                                                                    Score 186.5; DB 2;
Pred. No. 0.00011;
"Cmatches 65;
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Pred. No. 0.00026;
32; Mismatches 74;
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Shiba, T.; Hattori, M
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Shinagawa,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE000206; GB:U00096; NID:g1787282; PIDN:AAC74129.1; PID:g1787283 A;Experimental source: strain K-12, substrain MG1655 C;Superfamily: Pyrococcus abyssi hypothetical protein PAB0445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 277, 1453-1462, 1997

A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: B64847
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: C85666
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: B64847
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C; Species: Escherichia coli
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A;Experimental source: strain 0157:H7, substrain EDL933
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A; Residues: 1-177 <STO>
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                                                                                                                                 PALSSGIFQFPLNLCTKTIVETI 259
                                                                                      PAISTGVYGYPRAAAAEIAVKTV 141
                                                                                                                                                                               TGHAVITLAGDLPAKAVVHTVGPVW-RGGEQNEDQLLQDAYLNSLRLVAANS--YTSVAF 118
                                                                                                                                                                                                                          AGEIAVTGAGRLPCKOIIHAVGPRWMEWDKQGCTGKLQRAIVSILNYVIYKNTHIKTVAI 236
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    Mayhew Apodaca,
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C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: H75106
R:anonymous, Genoscope
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A;Molecule type: DNA
A;Residues: 1-186 <KAND
A;Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49569.1; PID:g545
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A; Accession: H75106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein PAB0445 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: PAB0445
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                                         KTVAIPALSSGIFQFPLNLCTKTIVETIRVSLQGKPMMSNLKEIHLV--SNEDPTVA 286
                                                                                                                                                                                    DITREKAEAIVNAANKYLEHGGGVAYAIAKAASGDVSEYIRISKEEMRKQIGR-DWIEHG
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                                                                                                                                    EIAVT---GAGRLPCKQIIHAVGP----RWMEWDKQGCTGKLQRAIVSILNYVIYKNTHI
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57; Conserv
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YR50_LISMO
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Y0J3_PSEAE
YMDB_SALTY
YF13_PYRAO
Y189_MYCTU
YMDB_ECOLI
Y445_PYRAB
Y189_STRGO
Y189_STRGFU
YMDB_ECOLI
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YHTEVO
Y189_THEVO
Y189_THEVO
Y189_THEWO
Y189_TREMD
H2AY_HUMAN
Y987_AQUAE
H2AY_RAT
RRPA_CVH22
SMC_METJA
YG48_AERPE
YM88_DEIRA
POLN_EEVV3
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Q9zbg3 streptomyce
Q9ey16 streptomyce
Q07733 mycobacteri
P75918 escherichia
 Q9v0y3
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Q28751
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Q9h167
Q9716
Q93r9
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Q067112
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Q09ybe9
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P27282
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Q96xy5 sulfolobus
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2 aquifex aeo
4 rattus norv
2 human.coron
7 methanococc
9 aeropyrum p
9 deinococcus
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2 streptomyce
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7 pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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STRAIN-ANCC 35092 / DSM 1617 / P2;

MEDLINE-21332296; PubMed-11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G., Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A., De Moors A., Erauso G., Fletcher C., Gordon P.M.K., Medina N., Peng X. Thirmage de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X. Thirmagoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N., Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T., Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus | Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
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                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical SEQUENCE 17
                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01661; Alpp; 1
SMART; SM00506; Alpp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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15-JUN-2002
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                                                                                                                             5-JUN-2002
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                                                                                                                                                          236 IPALSSGIFQFPLNLCTKTIVETIR
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                                                                                                                                                                                                                                                                                                                     59;
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(Rel. 41, Last sequence up
(Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                     Conservative
                                               STANDARD;
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                  Score 288; DB 1;
Pred. No. 2.7e-11;
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                                                                                                                              144
                                                                                                                                                            260
                                                                                                                                                                                                                                                                                                                                                                                  proteome.
8353685B14FECA96 CRC64;
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Created) Last sequence

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RESULT
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Best Local
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Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baguero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Last sequence update)
Hypothetical protein Lmo2759.
LMO2759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01.661; Alpp; 1.
Hypothetical protein; Complete
SEQUENCE 182 AA; 19369 MW;
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                                                                                                                                                                                                                                                                                                                                 LISMO
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                                                                                                                     STRAIN=EGD-e / Serovar
MEDLINE=21537279; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the hyperthermophilic orenarchaeon aerophilum.";
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                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                               NCBI_TaxID=1639;
                                                                                                                                                                                               Listeria monocytogenes
Bacteria; Firmicutes; |
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15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
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Q8Y3S3;
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SIMILARITY: BELONGS TO THE UPF0189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEVVLMRGDITEVEADAIVNAANSYLEHGGGVAGAIVRKGGQVIQEESREWVRKHGPVPV 67
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37.2%;
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E UPF0189 FAMILY.
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3158ADD9C243EF3E CRC64;
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RESULT 6
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Best Local S
Matches 55
                                                                                                          Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T., Charriet A., Chetouani F., Couve E., de Darvar A., Dehoux P., Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget (Entian K.-D., Fshhi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson I. Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell I., Nemmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Varapez-Boland J.-A., Voss H., Wehland J., Cossart P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002589; Alpp.
Pfam; PF01661; Alpp; 1.
Hypothetical protein; Complete SEQUENCE 176 AA; 18984 MW;
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CLIP 11262 / Serovar 6a;
MEDLINE=21537279; PubMed=11679669;
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          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                  Science 294:849-852(2001).
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15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Hypothetical protein Lin2902.
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                                                                                              "Comparative genomics of Listeria
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| 55; | Conser
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Pred. No. 5.3e
99; Mismatches
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3362EA4DA723050B CRC64;
                                                                                              species.";
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                                                              FAMILY.
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                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             "The shuffling function of resolvases."; Gene 269:121-130(2001).
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15-JUN-2002 (Rel. 41, Last annotation u
Hypothetical 20.0 kDa protein (ORF549).
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                                                                                                                                                    Hypothetical protein;
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                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21272500; PubMed=11376944;
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186
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GRLPCKQIIHAVGPRWMEWDKQGCTGKLQRAIVSILNYVIYK--NTHIKTVAIPALSSGI 24:
                                                   DLTTHAVDAVVNAANEDLLHGGGLALALVKAGGFEIQEESKQFVARYGKVSAGEIAVTGA 185
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                         DITAFAVHAIVNSANKSLLGGGGLDYVIHKKAGPLMKEECVRLNQEKGGCPTGQAEVTTA
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                                                                                                                                                               PF01661; A1pp;
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Pred. No. 1
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Pred. No. 8.1e-08
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7F135271F4499159 CRC64;
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RESULT 9
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YGB2_ALCEU
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Q9HXU7;
15-JUN-2002
15-JUN-2002
15-JUN-2002
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15-JUN-2002
15-JUN-2002
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Pfam; PF01661; Alpp; 1
SMART; SM00506; Alpp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valentin H.E., Zwingmann G., Schoenebaum A., Steinbuechel A.; "Metabolic pathway for biosynthesis of poly(3-hydroxybutyrate) from 4-hydroxybutyrate by Alcaligenes eutrophus."; Eur. J. Biochem. 227:43-60(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-H16 / SK4040;
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Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                        Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical SEQUENCE 1
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                              PA3693
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                                                                                                                                                                                                                                      AVITTGGHLPAPYVIHAVGPVWQGGD-QGEDELLANA----
                                                                                                                                                                                                                                                                                          LQVVHGDITRMEVDAIVNAANSGLLGGGGVDGAIHGAGGSAIKEACRAIRDTQGGCPTGE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGFPPQKAAETAIGTI---LSMLPQYDHVAEVFFICREDENYLIYK 167
                                                                                                                                                                                                                                                                                                                                                57;
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173 AA; 1
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(Rel. 41, Last sequence up
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                                        protein PA3693.
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Pred. No. '
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagro Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Pauling I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V., "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
                                                                                                                                                                                                                                                                                                                                                                                                            Q8ZQ29; Q8Z7M1;
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Hypothetical protein ymdB.
YMDB OR STM1147 OR STY1184.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The structions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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MEDLINE=20437337; PubMed=
                         McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courthey L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
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                                                                                                                                                                  SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                     SEQUENCE
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EMBL; AL627269; CAD08271.1; ALT_1
StyGene; SG????; ymdB.
InterPro; IPR002589; Alpp.
Pfam; PF01661; Alpp; 1.
Hypothetical protein; Complete p.
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15-JUN-2002
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=S.typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D.,
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Oh
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18."; Nature 413:848-652(2001).
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                                                                           STRAIN=OT3
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"Genome sequence of the plant pathogen Ralstonia solanacearum Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aoki K.-I., Yoshizawa T., Nakamura Y., Ro
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the sequence and gene organization of the sequence archaebacterium, Pyrococcus
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                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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-!- SIMILARITY: BELONGS TO THE UPF0189 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF01661; Alpp; 1.
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hetical protein; Complete
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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  Bioinformatics
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  Institute.
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                                                                                                        FAMILY.
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Schiex T.,
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                          EMBL outstation
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Best Local S
Matches 52
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Hypothetical protein SCO6450.
SCO6450 OR SC9B5.17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Seeger K., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restricted the succession of the succession
                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of the model actinomycete coelicolor A3(2).";
Nature 417:141-147(2002).
-i- SIMILARITY: BELONGS TO THE UPF0189 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002589; Alpp.
Pfam; PF01661; Alpp; 1.
Hypothetical protein; Complete
SEQUENCE 171 AA; 18018 MW;
                                                                        InterPro: IPR002589; Alpp. Pfam; PF01661; Alpp; 1.
                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed
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MEDLINE=21996410; PubMed=12000953;
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                                                                                                                               EMBL; AL035206; CAA22759.1;
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                                                                                                                                                                                    email to license@isb-sib.ch)
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Hypothetical protein; SEQUENCE 169 AA; 1

n; Complete 17767 MW;

proteome. 86965DB33C6E4740 CRC64;

SMART; SM00506; Alpp; 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRNO
                                                                                                                                                                                                                                                  InterPro; IPR002589; Alpp. Pfam; PF01661; Alpp; 1. SMART; SM00506; Alpp; 1.
                                                                                                                                                                                                                                                                                                                                                    the European Bloinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteria (class); Ac Actinomycetales; Streptomycineae; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                  entitles requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nogalater: characterization
hybrid structures.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 27451;
MEDLINE=21539456; PubMed=11683270;
                                                                                                                                                                                                                                                                                               EMBL; AF323753; AAG42849.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The entire nogalamycin biosynthetic nogalater: characterization of a 20-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ylihonko K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Torkkell S., Kunnari T., Palmu K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE UPF0189 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119
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                                                                                                                             LSVWKDDLTTHAVDAVVNAANEDLLHGGGLALALVKAGGFEIQEESKQF-VARYGK-VSA 177
                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAISTGVYRWPMDDAARIAVETVATT -----KTSVTEIRFVLFDARAYEAFAA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PALSSGIFQFPLNLCTKTIVETIRVSLQGKPMMSNLKEIHLVSNEDPTVAAFKA
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 PALSTGVYRWPMGDAARIAVETVRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genet. Genomics 266:276-288(2001)
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                          PALSSGIFQFPLNLCTKTIVETIRVS
                                                      GRAVATTAGDLDARWVIHTVGPVWSSTEDRSDLLASCYRESLRLAG----
                                                                                GEIAVTGAGRLPCKQIIHAVGPRWMEW-DKQGCTGKLQRAIVSILNYVIYKNTHIKTVAI 236
                                                                                                              ITLVQGDITRQHADALVNAANSSLLGGGGVDGAIHRRGGPAILAECRALRASRYGEGLPT
                                                                                                                                                                      Similarity 48; Conser
                                                                                                                                                                                                                           181 AA;
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                                                                                                                                                                      Conservative
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32.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 193; DB 1;
Pred. No. 2.2e-05;
8; Mismatches 62;
                                                                                                                                                                                                                           C91684D0A793F4CA CRC64;
144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cluster
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                                                                                                                                                                                             Length 181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Streptomyces
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                                                      -ELGARTVAF
                                                                                                                                                                                                                                                                                                                                                                                              EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                a collaboration
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pb Qq

118 IELSVWKDDLTTHAVDAVVNAANEDLLHGGGLALALVKAGGFEIQEESKQFVARYGKVSA 177

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190

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RESULT 15
VI19_MY
ID YI19_M
AC 007733
DT 15-JUN
CHICAL
GN RV1899
OS Mycoba
OC Actino
OX Mycoba
OC Actino
OX MYCOL
RR COL
RR COLL
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RR GOIDON
RA FLEIS
RA FLEIS
CC This I
CC 
                                Best
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TIGR; M7195,
Tuberculist; Rv1899c;
InterPro, IPR002589; Alpp.
InterPro, IPR002589; Alpp.
Pfam; PF01661; Alpp; 1.
SMART; SW00506; Alpp; 1.
SMART; SW00506; Alpp; 1.
UNKNOWN.
184
UPF0189.
ALPAVA/
                                                   Query Match
        Matches
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequenc
15-JUN-2002 (Rel. 41, Last annotat
Hypothetical protein Rv1899c.
RV1899C OR MT1950 OR MTCY180.19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C., Eiglmeier R., Gas S., Barry C., Eiglmeier R., Gas S., Barry C., Eiglmeier R., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White
Fleischmann R.D., Hickey
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzbe
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mi
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 297193; CAB10035.1; ALT_INIT. EMBL; AE007050; AAK46221.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement (Seentities requires a license agreement (Seentities requires a license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE UPF0189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis
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                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole genome comparison of Mycobacterium tuberculosis clinical
                                Local
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                             Similarity
                                                                                                            359 AA;
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126
        Conservative
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                             4.2%;
29.0%;
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        32;
                                                                                                       A -> ALPAVAASTARPAATA (IN REF. C -> S (IN REF. 2). F7E3BB74F35B1426 CRC64;
Pred. No. 0.00
2; Mismatches
                           Score 187.5;
Pred. No. 0.
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        0.00013;
les 74;
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J., Mikula A.,
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Sear Job	Db	Оу	DЬ	Qy	Db	Qy
Search completed: May 13, 2003, 11:42:45 Job time : 31 secs	b 350 IQAGEDT 356	293 EFILGKS	b 296 SLALVAFGTGVGGFPLDDAARLMVGAVRRHRPGSLQRVVFAVHGDAAERAFSAA- 349	233	b 246 GEAVETTAGDMPARYVIHAATMELGGPTSGEIITAATAATLRKADELGCR 295	178 GEIAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTG
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                              4220.5
2453
1747
610
  . 420
256
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230.5
211.5
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1: sp_archea:*
2: sp_bacteria
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4447
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Match Length DB
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9::
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Gapop 10.0 , Gapext 0.5
   MDFSMVAGAAAYNEKSGRIT.....pmRPFAQHPWRGFASGSPVD 854
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                                                                                                                                                                                                                                                                                                       sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                  sp_organelle:*
sp_phage:*
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sp_rodent:*
                                                                                                       854
819
830
330
1023
556
419
                        424
183
1025
672
393
Q8RB30
Q8QGB0
Q8VDT6
Q8U0P9
Q96K72
Q8WV05
Q96CH7
Q948R9
Q8R133
                                                                                                       Q9BZL9
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L Q99LF9
Q8TCP3
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                               O9bz19 homo sapien
O9bz18 homo sapien
O9bz18 homo sapien
O991f9 mus musculu
O8tcp3 homo sapien
O9ulf2 homo sapien
O9ulf2 homo sapien
O9h9x9 homo sapien
O8rb30 thermoanaer
O8gpb0 oncorhynchu
O8wdt6 mus musculu
O8wdt6 mus musculu
O8wdp9 pyrococcus
O96k72 homo sapien
O8wv05 homo sapien
                       Q96k72
Q8wv05
Q96ch7
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            09h8r9
  Q8r133
          homo
sapien
sapien
musculu
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45	44	43	42	41	40	39	38	37	36	35	34	<b>ω</b>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
156	156	156	156.5	157.5	157.5	159.5	159.5	159.5	159.5	160	160.5	161.5	161.5	165.5	166	168	171.5	176	177	178	182	182	186.5	189	190	190	195.5	197
ა ა	ω .5	3 5	3 5	3 .5	3 5	3.6	3.6	3.6	3.6	3.6	3.6	ω. 6	ω. 6	3.7	3.7	3.8	3.9	4.0	4.0	4.0	4.1	4.1	4.2	4.3	4.3	4.3	4.4	4.4
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Q9nti3 homo sapien	009140 rattus norv	Q9h610 homo sapien	Q9qzq8 mus musculu	Q9vbp3 drosophila	Q9xz37 drosophila		bovine		Q91a28 bovine coro	Q17432 caenorhabdi	Q9wjd0 venezuelan	Q96d41 homo sapien	5				Q8twt2 methanopyru				Q922b1 mus musculu	Q8tqd0 methanosarc	2 fusc		homo	homo	Q8taj3 homo sapien	Q8rlu9 mus musculu

# ALIGNMENTS

Qy Db Qy	Qu Be Ma	SQ	DR	DR		RE	RT	χŢ	RA	RA	RX	RP	RN	o <sub>x</sub>	8	8	20	GN N	DE	PΤ	DT	DŢ	AC	ID	RESULT 09BZL9
1 MDESMVAGAAAYNEKSGRITSLSLLFQKVFAQIFPQWRKGNTEECLPYKCSETGALGENY 60	Query Match 99.8%; Score 4438; DB 4; Length 854; Best Local Similarity 99.9%; Pred. No. 4.5e-301; Matches 853; Conservative 0; Mismatches 1; Indels 0; Gaps C	SEQUENCE 854 AA; 96283 MW; E80663868ECDECD3 CRC64;	SMART; SM00506; Alpp; 2.	Pfam; PF01661; Alpp; 2.	TSTONTON TIBERONISTON AND CONTROL OF TSTONTON TO TSTONTON	Blood 96:4328-4334(2000).		"BAL is a novel risk-related gene in diffuse large B-cell lymphomas		Aguiar R.C.T., Yakushijin Y., Kharbanda S., Salgia R., Fletcher J.A.,	MEDLINE=20563954; PubMed=11110709; .	SEQUENCE FROM N.A.	[1]			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).		onq	(TrEMBLrel. 19,	(TrEMBLrel. 17,	01-JUN-2001 (TremBLrel. 17, Created)	••	Q9BZL9 PRELIMINARY; PRT; 854 AA.	LT 1
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Aguiar R.C.T., Yakushijin Y., Khar
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Mammalia; Eutheria; Primates;
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EMBL; AF307339; AAK07559.1; -
InterPro; IPR002589; Alpp.
Pfam; PF01661; Alpp; 2.

SMART; SM00506; Alpp; 2.

SEQUENCE 819 AA; 92211 MW;
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les 818; Conservative
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InterPro; IPR002589; A1pp.
InterPro; IPR001901; SecE.
Pfam; pP01661; A1pp; 2.
PMART; SM00506; A1pp; 2.
SMART; SM00506; A1pp; 2.
PROSITE; PS011067; SECE_SEC61G; UI Hypothetical protein.
SEQUENCE 830 AA; 92669 MW; 7.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 92.7 kDa protein.
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Submitted (F
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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KL-DKMEESYTFQRYPASCTQELQDRKKQFEKCGLWVVQVEQIDNKVLLAAFQEKKKMME
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                                        KTQDEMKENIIFLKCPVPPTQELLDQKKQFEKCGLQVLKVEKIDNEVLMAAFQRKKKMME
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Pred. No. 1.6e-162;
6; Mismatches 206;
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Q9ULF2;
01-MAY-2000
01-MAY-2000
01-JUN-2002
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                                   Q9ULF2
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TISSUE=AMYGDALA;
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                                                                              YVQSQDYSSGPMRPFAQHPWRGFASGSPVD
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(TrEMBLrel. 13, 12) (TrEMBLrel. 13, 12) (TrEMBLrel. 21, 13)
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                                   PRELIMINARY;
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; Pred. No. 7.2e-114;
0; Mismatches 0;
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Catarrhini; Hominidae
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Pfam; PF02825; WWE; 1.
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Nagase T., Ishikawa K., Kikuno R., Hirosawa M., Nomura N.,
"Prediction of the coding sequences of unidentified human c
The complete sequences of 100 new cDNA clones from brain when the complete sequences of 100 new cDNA clones from brain when the complete sequences of 100 new cDNA clones from brain when the complete sequences of 100 new cDNA clones from brain when the complete sequences of 100 new cDNA clones from brain when the complete sequences of 100 new cDNA clones from brain when the complete sequences of 100 new cDNA clones from brain when the complete sequences of 100 new cDNA clones from brain when the complete sequences of 100 new cDNA clones from brain when the complete sequences of 100 new cDNA clones from brain when the complete sequences of 100 new cDNA clones from brain when the complete sequences of 100 new cDNA clones from brain when the complete sequences of 100 new cDNA clones from brain when the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones from the clones from the clones from the clones from the clones from th
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Mammalia; Eutheria;
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IIFLKCPVPPTQELLDQKK----QFEKCGLQVLKVE
                                                                   IDA----IEDFVQKGSAQSVKKVKVVIFLPQVLDVFYANMKKREGTQLSSQQSVMSKLASF
                                                                                                                                                                                                           TGGGFLRCKNIIHVIGGNDVKSSVSSVLQECEKKNYSSICLPAIGTGNAKQHPDKVAEAI
                                                                                                                                                                                                                                                                       ENN------GRTELEIEGARADL
                                                                                                                                                                                                                                                                                                                                                  GDITKEE-ADVIVNSTSNSFNLKAGVSKAILECAGQNVERECS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDHENIQAFSDEFARRANGNLVSDKIPKAKDTQGFYGTVSSPDSGVYEMKIGSIIFQVAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ELGQETTPSENAMVVNNLTLQIVQGHIEWQTADVIVNSVNPHDITV--GPVAKSILQQA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENFQFKKDGHCLKEIYLVDVSEKTVEAFAEAVKTVFKATLPDTAAPPGLPPAAAGPGKTS
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AB033094; BAA86582.1; -.
Pro; IPR002589; Alpp.
Pro; IPR004170; WWE_dom.
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Primates;
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29.0%;
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Pred. No. 9.9e
13; Mismatches
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.9e-34;
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01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Kanehori K.;
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SMART; SM00506; Alpp; 2.
NON_TER 556 556
SEQUENCE 556 AA; 62079 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "NEDO human cDNA sequencing pr
Submitted (FEB-2000) to the EM
EMBL; AK001770; BAA91897.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=OVARIAN CARCINOMA;
ISOgai T., Ota T., Hayashi K.,
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InterPro; IPR004170; WWE_dom
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GRKEHDILSQLQKTSSVSITEIISPGRTELEIEGARADLIEVVMNIEDMLCKVQEEMARK
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                                         -KQSPQKKNHLVLEKKTESATFRVCGENVTCVEYAISWLQDLIEKEQCPYTSEDECIKDF
                                                                      PQSTREEKRENGLEAR--SPAINLMGFNVEEMYEAHAWIQRILSL-QNHHIIENNHILYL
                                                                                                     AIEDFVQKGSAQSVKKVKVVIFLPQVLDVFYANMKKREGTQLSSQQSVMSKLASFLGFS-
                                                                                                                               EVLTFA-KDHVKHQLTVKFVIF-PTDLEIYKA----
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 118;
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26.6%;
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EMBL/GenBank/DDBJ databases
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RESULT
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Q9RB30;
01-JUN-2002
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09H9X9;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ
EMBL; AK022542; BAB14089.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Ninomiya K., Iwayanagi T.;
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                                                                                            VLTGIYTHGNHSLIVPPSKNPQNPTDLYDTVTDNVHHPSLFVAFYDYQAYPEYLIT
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                           PRELIMINARY;
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ORGGBO;
Ol-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Ol-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Ol-JUN-2002 (TrEMBLrel. 21, Last annotation update)
VHSV-induced protein-10.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
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"A complete sequence of T. tengcongensis genome."; Genome Res. 12:689-700(2002).
EMBL; AE013064; AMM24250.1; -
Hypothetical protein; Complete proteome.
BYPOTHEM TO THE PROTECT OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Benmansour A., Boubinot P., Vaghefi N., O'Farrell C.; "Global Survey of Transcript Expression in Rainbow Trout Leukocytes Reveals a Major Contribution of Interferon Responsive Genes in the Early Response to a Rhabdovirus Infection."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanae
NCBI_TaxID=119072;
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KNKHTNNEKLLFHGTSSDSITQINNHGFNRSYAGTHGAAIGNGSYFAVNSSYSARGYSKA
                                                                  KLHROPVSHRLFQQVPYQFCNVVCRVGFQRMYSTPCDPKYGAGIYFTKNLKNLAEKAKKI
                                                                                                                                            DDMKGSLLMLVPLTPGSKEGHDIEKEFRKTLLNNTILTIERVQNDSLWKSYQIRKKLLEE
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DT 01-JUN-2002 (TrEMBLrel. 20, Last sequence update)
DE Hypothetical 48.4 kDa protein.
S Mus musculus (Mouse).
C Eukaryota: Metazoa; Chordata; Craniata: V^~-^*
Mammalia; Eutheria; Rodentia- ^-
NCBI_TaxID-1000^^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Ma
Best Loc
Matches
                                         01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JAP-2002) to the EMBL/GenBank/DDBJ
EMBL; BC021340; AAH21340.1; -
InterPro; IPR004170; WWE_dom.
Pfam; PF02825; WWE; 1.
                                                                                                              Q8U0P9;
                                                                                                                                       Q8U0P9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. SEQUENCE 424 AA; 4
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Hypothetical PF1536.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262
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es 92; Conserv
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                                                                                                                                                                                                                                                      VLTGNYTNGNASLIVPPSRDPQNAADLYDTVTDNDKNPSIFVVFYDNQTYPEYLITFRQ
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              2 (TrEMBLrel. 2 (TrEMBLrel. 2 (TrEMBLrel. 2 )
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                                                                                                                                    PRELIMINARY;
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el. 21,
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Pred. No. 7.7e
70; Mismatches
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                                                                                         Created)
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                                             annotation
                                                                 sequence
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                                         update)
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Best Local :
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Q96K72;
01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-MAMMARY GLAND;
TISSUE-MAMMARY GLAND;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara N.
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.
Watahabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK027370; BAB55067.1; -.
SEQUENCE 1025 AA; 109884 MW; 87C4DBB8F42DB84C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422; Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.; "The complete sequence of the Pyrococcus furiosus Submitted (FEB-2002) to the EMBL/GenBank/DDBJ data EMBL, AE010254; AAL81660.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus.
NCBI_TaxID=2261;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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  311
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  GPIVQGRGIMTTGSGQEPGQSGTSLRTGP
                                                GKVSAGE-IAVTGAGRLPCKQ-IIHAVGPRWMEWDKQGCTGKLQRAIVSILNYVIYKNTH
                                                                                                                                                                                                         NERRSGGGPLEDLQRLPGPLGTVASFQQWQVAERVLQQEHRLQGSELSLVPHYDVLEPEE
                                                                                                                                                                                                                                                          NERQL----CEVLQNKFGCISTLVSPVQ------EGNSKSLQVFRKMLTPR-
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                                                                                                   LAENTSGGDHPSTQGPRATKHA-----LLRTGGLVTALQGAGTVTMGSGEEPGQSGASLRT
                                                                                                                                                   -IELSVWKDDLTTHAVDAVVNAANEDLLHGGGLALALVKAGGFEI--QEESKQFVA--RY
                                                                                                                                                                                                                                                                                                                194;
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94; Conservative
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
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Pred.
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                        Score 211.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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SEQUENCE
                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21, Similar to hypothetical protessions)
                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                       Similar to "Ir".
Homo sapiens (Human).
Chordata;
Chordata;
Hypothetical protein.
NON_TER 1
SEQUENCE 393 AA; 4
                                        Submitted (SEP-2001) to the EMBL; BC014229; AAH14229.1;
                                                                  Strausberg R.;
                                                                                   TISSUE=SKIN;
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 639
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                                                                                                                                                                                                                                                                                                                                        SGMQAIPQYLWTCTQEYVQSQDYSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQKTQDEMKENIIFLKCPVPPTQELLDQKKQFEKCGLQVLKVEKIDNEVLMAAFQRKKKM
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24; Conservative 103;
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                                                                                                                                                                                                                                              PRELIMINARY;
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19.8%;
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  43199
                                                                                                                                                                       19, Last sequence update)
21, Last annotation update)
protein FLJ14464 (Fragment).
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Pred. No. 6.9e-
03; Mismatches
                                                    EMBL/GenBank/DDBJ
                                                                                                                                                                                                                 Created)
                                                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae
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 A7D1B75AB684DC26
                                                                                                                                                                                                                                                                                                                 664
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es 281;
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Query Match Best Local Similarity Matches 87; Conserv

Conservative

4.6%;

; Score 205; DB 4; Length 39; Pred. No. 4.1e-06; 63; Mismatches 179; Indels

Length 393;

Gaps

10;

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RESULT 15
Q9H8R9
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Best Local Similarity
Tatches 68; Conserve
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                                                                                                                                                                                                           Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Mas Minomiya K., Iwayanagi T.;
"NEDO himan cDNA sequencing project.";
submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK023350; BAB14537.1;
InterPro; IPR001230; Prenyl_site.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SEQUENCE 363 AA; 42107 MW; 8048C4D40D231F85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
0VARC1001167 protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

TISSUE-OVARIAN CARCINOMA;

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Isogai T., Ota T., Hayashi K., Sugano S., Shiratori A., Sudo H.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

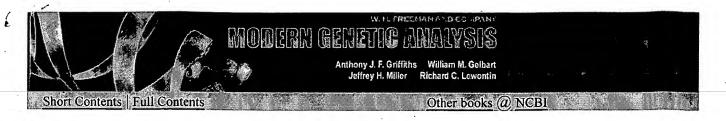
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                       128 IQTNIASKTQKDVIRRPTFVPQWYVQQMKRGPDHEPAKTSSVSLTATFRPQEDFCFLSSK 187
                                                                              607 VQEEMARKKERGLWRS---LGQWTIQQQK---TQDEMKENIIFLKCPVPPTQE--LLDQK 658
                     659 K-----
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                                                                                                                                    Conservative
                                                                                                                                                   4.6%;
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            834
-QFEKCGLQVLKVE---KIDNEVLMAAFQRKKKMMEEKLHRQP 698
                                                                                                                                  33;
                                                                                                                                                   Score 203; DB 4
Pred. No. 5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 AA
                                                                                                                                                                   DB_4; Length 363;
                                                                                                                                                                                                                                                                                                                                                 Nagahari K., Masuho Y.,
                                                                                                                                    97;
                                                                                                                                  Indels
                                                                                                                                  52;
                                                                                                                                  Gaps
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Q Db δÕ ρy 밁 Ъ В 815 299 699 348 243 188 KYKLSEIHHLHPEYVRVSEHFKASMKNFKIEKIKKIENSELLDKFTWKKSQMKEE-----755 ADKLIYVFEAEVLTGFFCQGHPLNIVPPPLSPGAIDGHDSVVDNVSSPETFVIFSGMQAI 814 VSHRLFQQVPYQFCNVVCRVGFQRMYSTPCDPKYGAGIYFTKNL----KNLAEKAKKISA PQYVIEYTED PQYLWTCTQE 824 ----VVMFVAQVLVGKFTEGNITYTSPPP-----QFDSCVDTRSNPSVFVIFQKDQVY 347 -GKLLFYATSRAYVESICSNNFDSFLHETHENKYGKGIYFAKDAIYSHKNCPYDAKN---754 298 242

Search completed: May 13, 2003, 11:44:33 Job time: 105 secs



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Technology

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In Vitro Mutagenesis

#### RFLP Mapping

Reverse Genetics

Expressing
Eukaryotic
Genes in
Bacteria

Recombinant
DNA
Technology in
Eukaryotes

Gene Therapy

Using
Recombinant
DNA to Detect
Disease Alleles
Directly

Summary

Concept Map

Solved Problem

Solution

Solved Problem

**Problems** 

## Figures

Figure 11-2.

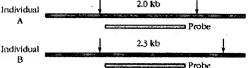
Mapping a gene...

Figure 11-3.
The detection and...

Search

# **RFLP Mapping**

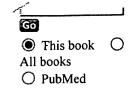
In Chapter 10, we learned that, if a cloned DNA fragment is used as a probe of genomic DNA that has been cut with a restriction enzyme, then the probe will bind to one or more genomic fragments. For example, if the restriction enzyme used does not cut within the chromosomal region encompassed by the cloned fragment, then the probe should bind to one fragment flanked by restriction sites on each side. Since the DNA of chromosomes within a species is generally homologous, it might be expected that a constant-sized genomic fragment will be bound in all individuals. However, when probes are used in this way, the bound fragments are often found to be of different sizes in different individuals. The explanation is that a given restriction site is not always found in all individuals. The absence of a site is usually caused by a single nucleotide difference that is most likely biologically neutral. Hence, for example, if a probe binds a 2-kb fragment in individual A of a haploid species and it binds a fragment of 2.3 kb in individual B, the reason is usually that one of the sites that flanked the 2-kb fragment is missing in B, and the next site is 0.3 kb away, making the hybridized fragment 2.3 kb in size.



The presence and absence of the restriction site can be treated as two alleles that can be thought of as + and - alleles. The presence of the + in some individuals in the population and the absence (-) in others generates a **restriction fragment length polymorphism,** or <u>RFLP.</u> (In the case just discussed, there was a dimorphism—two "morphs," one short and one long.) Geneticists were surprised to discover that RFLPs are quite common in populations and that a large proportion of probes will detect one. RFLPs are identified by a rather hit-or-miss method of hybridizing panels of randomly cloned genomic fragments to genomic restriction digests of several different individuals in a family or a population. Because RFLPs are a relatively common type of variation in nature, this method succeeds in finding RFLPs in most cases.

The significance of RFLPs is threefold. First, if an individual is heterozygous for two morphs of an RFLP, this heterozygous "locus" can be used as a marker in chromosomal mapping. Although at first the locus of the RFLP is not necessarily known, as more and more RFLPs are found, they can be mapped in relation to gene loci and in relation to other RFLP loci, and their positions gradually saturate the genetic map. The RFLPs are not biologically significant in most cases, but they can be used to map interesting genes and act as positions from which these

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genes can be cloned by positional cloning.

Second, in an extension of mapping analysis, RFLP alleles (morphs) can be used as diagnostic tools. For example, in a family with a record of a certain disease, if it can be established that the people who have the disease also carry a specific allele of an RFLP, then this fact suggests not only that the RFLP locus is linked to the disease gene locus, but furthermore that the specific RFLP allele is in cis arrangement with the disease allele. Hence the RFLP allele becomes a diagnostic marker for the disease, and this information can be used in genetic counseling.

Third, RFLPs can be used to measure genetic divergence between different populations or related species. The restriction-site difference is effectively a DNA difference, so a measure of the total number of RFLP differences represents a measure of genetic difference. Hence RFLPs are important in studies of evolution.

RFLP mapping is often performed on a defined set of strains or individuals that become "standards" for mapping that species. For example, in the fungus Neurospora, two wild-type strains, Oak Ridge and Mauriceville, are known to show many RFLP differences, so these strains have become standards used in RFLP mapping. The RFLPs can be mapped relative to one another or to genes of known phenotypic expression. For example, let ad stand for an allele for adenine requirement, and 1 and 2 stand for RFLP loci with either the Oak Ridge (OR) or Mauriceville (M) "alleles." A cross can be made of the type  $ad \cdot 1^{OR} \cdot 2^{OR} \times ad^+$ . 1<sup>M</sup> . 2<sup>M</sup> Progeny are tested for all three loci. Adenine requirement is tested by inoculating strains on medium lacking adenine, and the RFLP alleles are tested by probing with the relevant probes. Recombinant frequencies are calculated in the usual way. Most mutants in *Neurospora* have been induced in Oak Ridge wild-type strains, so it is a simple matter to map the mutant alleles to RFLPs simply by crossing the mutant Oak Ridge strain to the wild-type Mauriceville strain. An example of mapping a phenotypic mutant by using RFLP markers is shown in Figure 11-2.

Similar standard strains have been established in other organisms. An analogous approach has been used in human genome mapping by collecting DNA from a defined set of individuals in 61 families with an average of eight children per family and making this DNA available throughout the world to provide a standard for RFLP mapping.

Figure 11-3 shows an example of linkage of a human disease allele to an RFLP locus and the potential for using this information in diagnostics. Because of the close linkage, future generations of persons showing the RFLP morph 1 can be predicted to have a high chance of inheriting the disease allele D. This sort of predictive power can be used in prenatal diagnoses of the genotypes of fetuses, with the use of amniocentesis or chorionic villus sampling (considered later in this chapter).

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#### MESSAGE

RFLPs provide useful molecular marker loci for chromosome mapping and for diagnosis of human disease alleles.

It is worth comparing the process of making a restriction map (restriction mapping, pages 327–329) with the process of RFLP mapping. Restriction maps are based on physical analysis of DNA, whereas RFLP maps are based on recombination analysis of matings. Note also that restriction mapping is based on restriction sites with no variation, whereas RFLP mapping is based on restriction-site variation between homologous chromosomes. Most restriction maps are short-range (fine-scale) maps, although long-range maps can be constructed with rare-cutting restriction enzymes. In contrast, RFLP mapping generally produces long-range (coarse-scale) maps. RFLP mapping of whole genomes will be covered in detail in Chapter 12. • TOP

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